OM protein - protein search, using sw model

Run on: March 17, 2003, 08:44:41 ; Search time 13 Seconds
(without alignments)
2482.199 Million cell updates/sec

Title: US-10-010-227-3
Perfect score: 4055
Sequence: 1 MPGAESTPQTLYDKVLQAHV..........KAVPVPTTNRGEEKPEPLEW 778
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 100 summaries
Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2682.5	66.2	755	1	LEU2_RHIPU	P55251 rhizomucor
2	2546	62.8	750	1	LEU2_RHINI	P58811 rhizopus ni
3	2543	62.7	744	1	LEU2_PHYBL	P12250 phycomyces
4	2492.5	61.5	773	1	LEU2_USTMA	P49601 ustilago ma
5	2473.5	61.0	758	1	LEU2_SCHPO	O14289 schizosacch
6	2456.5	60.6	779	1	LEU2_YEAST	P07264 saccharomyc
7	2417.5	59.6	770	1	LEU2_CANMA	Q00464 candida mal
8	2076	51.2	644	1	LEU2_RHIRA	P17279 rhizomucor
9	1636	40.3	469	1	LEU2_RHIME	Q92176 rhizobium m
10	1611	39.7	469	1	LEU2_BRUME	Q8YIC9 brucella me
11	1584	39.1	469	1	LEU2_AGRT5	Q8UBY9 agrobacteri
12	1567.5	38.7	469	1	LEU2_RHILO	Q98EF1 rhizobium l
13	1562	38.5	479	1	LEU2_CAUCR	Q9ABN0 caulobacter
14	1548.5	38.2	469	1	LEU2_NEIMB	Q9JZ15 neisseria m
15	1545	38.1	469	1	LEU2_NEIMA	Q9JU82 neisseria m
16	1522.5	37.5	479	1	LEU2_XANCP	P58949 xanthomonas
17	1514.5	37.3	479	1	LEU2_XANAC	P58948 xanthomonas
18	1507.5	37.2	479	1	LEU2_PSEAE	Q9HZA3 pseudomonas
19	1498.5	37.0	474	1	LEU2_XYLFA	Q9PAX0 xylella fas
20	1493	36.8	469	1	LEU2_RALSO	Q8XXX3 ralstonia s
21	1483.5	36.6	469	1	LEU2_ECOLI	P30127 escherichia
22	1477.5	36.4	465	1	LEU2_SALTI	P15717 salmonella
23	1477	36.4	465	1	LE21_SALTI	Q8Z912 salmonella
24	1471	36.3	465	1	LEU2_HAEIN	P44968 haemophilus
25	1469.5	36.2	465	1	LEU2_ECO57	Q8X800 escherichia
26	1452	35.8	468	1	LEU2_YERPE	Q8ZIH0 yersinia pe
27	1446.5	35.7	465	1	LEU2_PASMU	Q9CJN7 pasteurella
28	1425.5	35.2	476	1	LEU2_VIBCH	P56934 vibrio chol
29	1413	34.8	476	1	LEU2_BUCAI	Q9KEF0 buchnera ap
30	1399.5	34.5	467	1	LEU2_BUCAI	Q9K881 buchnera ap
31	1396	34.4	485	1	LEU2_ACTTI	O44427 actinoplane
32	1393.5	34.4	471	1	LEU2_BACHD	Q9KEF0 bacillus ha
33	1385.5	34.2	472	1	LEU2_BACSU	P00858 bacillus su
34	1385	34.2	473	1	LEU2_STRCO	O86534 streptomyce
34	1385	34.2	473	1	LEU2_MYCTU	O53237 mycobacteri
35	1354.5	33.4	466	1	LEU2_BUCDN	O85072 buchnera ap
36	1354	33.4	469	1	LEU2_BUCAP	O85065 buchnera ap
37	1354	33.4	476	1	LEU2_MYCLE	O33123 mycobacteri
38	1347.5	33.2	481	1	LEU2_CORGL	P48573 corynebacte
39	1330	32.8	471	1	LEU2_CORGL	P58946 corynebacte
40	1322.5	32.6	465	1	LEU2_BUCRP	P58945 buchnera ap
41	1311.5	32.2	470	1	LEU2_CAMJE	Q9PIW1 campylobact
42	1290.5	31.8	466	1	LEU2_BUCTS	O31293 buchnera ap
43	1283.5	31.7	462	1	LEU2_LISIN	Q92A26 listeria in
44	1282	31.6	456	1	LEU2_STAAM	Q99SJ3 staphylococ
45	1281	31.6	456	1	LEU2_STAAW	P58947 staphylococ
46	1279.5	31.6	462	1	LEU2_LISMO	Q8Y5R7 listeria mo
47	1278.5	31.6	466	1	LEU2_LISIN	Q8Y9B8 listeria in
48	1275.5	31.5	443	1	LEU2_BUCUM	Q9EV10 buchnera ap
49	1259.5	31.1	443	1	LEU2_BUCUO	Q9EV95 buchnera ap
50	1253.5	30.9	442	1	LEU2_BUCUN	Q9EVI3 buchnera ap
51	1252.5	30.9	443	1	LEU2_BUCUS	Q9EVH7 buchnera ap
52	1236.5	30.5	442	1	LEU2_BUCUH	Q9EVE0 buchnera ap
53	1227.5	30.3	443	1	LEU2_BUCUE	Q9EVH4 buchnera ap
54	1225.5	30.2	442	1	LEU2_BUCUD	Q9EVG2 buchnera ap
55	1217.5	30.0	473	1	LEU2_SALTY	Q8ZND5 salmonella
56	1211.5	29.8	444	1	LEU2_BUCML	Q9ZND5 buchnera ap
57	1209.5	29.8	456	1	LE21_THETH	Q9AIM3 thermus the
58	1194.5	29.1	468	1	LEU2_STRGN	Q9AIM3 strepto coc
59	1181.5	29.1	467	1	LEU2_SYNY3	P54384 synechocyst
60	1172.5	28.9	460	1	LEU2_ANASP	Q8YX02 anabaena sp
61	1132.5	27.9	470	1	LEU2_LACLA	Q02142 lactococcus
62	1066	26.3	369	1	LEU2_AZOVI	P96195 azotobacter
63	1065.5	26.3	470	1	LEU2_BUCUL	Q9AGC6 buchnera ap
64	699.5	17.3	418	1	LEU2_METKA	Q8TVE2 methanopyru
65	684.5	16.9	424	1	LEU2_METJA	P81291 methanococc
66	662.5	16.3	432	1	LEU2_THETH	Q9UZ07 thermotoga
67	660	16.3	267	1	LEU2_METAC	Q8VMA6 rhizobium e
68	656.5	16.2	424	1	LEU2_RHIET	O27439 methanobact
69	641	15.8	431	1	LEU2_DEIRA	Q58409 methanococc
70	637.5	15.7	423	1	LE21_PYRAB	Q9W224 thermotoga
71	635	15.7	424	1	LE21_METKA	Q28316 archaeoglob
72	627.5	15.5	174	1	LEU2_METJA	Q92412 emericella
73	613	15.1	419	1	LEU2_RHIET	Q97EE0 clostridium
74	602.5	14.9	420	1	LEU2_METTH	O28084 archaeoglob
75	595.5	14.7	417	1	LE21_METJA	Q8TG23 methanosarc
76	587.5	14.5	418	1	LE22_THEMA	O27668 methanobact
77	584.5	14.4	775	1	LE21_ARCFU	Q02144 methanosarc
78	576.5	14.2	418	1	LYS4_EMENI	Q99798 homo sapien
79	573.5	14.1	434	1	LEU2_CLOAB	P34455 caenorhabdi
80	562	13.9	418	1	LEU2_ARCFU	P94568 bacillus su
81	552	13.6	201	1	LEU2_METAC	P16276 bacillus su
82	541.5	13.4	200	1	LE22_ARCFU	P20004 sus scrofa
83	539	13.3	418	1	LEU2_METAC	P20000 bos taurus
84	532.5	13.3	416	1	LEU2_METTH	Q9ZNE0 deinococcus
85	523.5	13.1	422	1	LE21_THEMA	Q9RY9 thermus the
86	512	12.9	416	1	LYS4_YEAST	P49367 saccharomyc
87	511.5	12.6	434	1	LEU2_AZOVI	P96196 azotobacter
88	505	12.6	418	1	LEU2_THERM	Q9RY9 thermus the
89	495	12.5	200	1	LE21_DEIRA	Q9ZNE0 deinococcus
90	491	12.2	191	1	LEU2_THETN	Q8RCK2 thermoanaer
91	482.5	12.1	201	1	LEU2_SALTY	P04787 salmonella
92	482.5	11.9	201	1	LEU2_HAEIN	P44438 haemophilus
93	475	11.9	199	1	LEU2_ECOLI	P30126 escherichia
94	466.5	11.7	777	1	LEU2_LACLA	P30126 lactococcus
95	462.5	11.5	780	1	LEUD_LACLA	Q99798 lactococcus
96	454.5	11.4	780	1	LEU2_HUMAN	Q02144 homo sapien
97	447	11.2	781	1	LEU2_CAEEL	P34455 caenorhabdi
98	444.5	11.0	415	1	LEUD_BACSU	P94568 bacillus su
99	443.5	11.0	789	1	LEUD_PIG	P20004 sus scrofa
100	441	10.9	779	1	ACON_BOVIN	P20000 bos taurus
		10.9	779	1	LEU2_PYRAE	P49609 pyrobaculum
				1	ACON_YEAST	P39533 saccharomyc
				1	ACOX_YEAST	Q8ZW41 saccharomyc
				1	ACON_GRAVE	P49609 gracilaria
		10.9	402	1	LE22_METKA	Q8TW29 methanopyru

RESULT 1

ALIGNMENTS

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Qy  189 GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD 248
        ||:||:|||:||||||||||||| ||||||||||||||||:||||||||:|||||||||||
Db  183 GVTSKDIVLHIIGVIGTAGGTGCVIEFCGSAFQMSMEARMSVCNMSIEAGARAGMIAPD 242

Qy  249 EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKXYDIDVFIDAKDIVPLTWGTSP 308
        | ||||:|:|||||    ||||:||||:||| ::||||:|:||:||||||:|||:|||||||
Db  243 ETTFEYIRGRPLAP--TGAEWDKAVEYWRSLRSDPDAKYDVDVFIDAADIAPTLTWGTSP 300

Qy  309 EDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIED 368
        :|||:||| ||||.||.:|:::||::|::::::||||:|||:|:|:|||||||||||||||
Db  301 QDVVAITGTTPDPSTVSDPIRRQAMERALDYIGLKPNTPMQEVKIDKVFIGSCTNSRIED 360

Qy  369 LRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGM 428
        |||||| |:||:|| || |||||||||||||:|||:|||::||:|||:|||||||||||||
Db  361 LRAAAATAKGRHVADWV-YAMVVPGSGLVKKQAEQEGLDRIFKEAGFDWREAGCSMCLGM 419

Qy  429 NPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKLT----DYK 484
        |||:| |:||||||||||||||||||||||||||.||||||.:.|::|||||||     |
Db  420 NPDQLKPGERCASTSNRNFEGRQGAGGRTHLMSPAMAAAAAVTGYFTDVRKLTPAQQDRP 479

Qy  485 ASPHIAAYQKSTVTKPHVDERINQDAHEKDIIADIPEDNNGPHTNSASVGTSAGLPKFT 544
        |||    .::.:. || ||:|| :|| |.|||.|:|.:: .  :|.:|.:.:.|:|||||
Db  480 ASP--TPKKIETELEPPVEDHA-KAADQADIVTDAPATGASP---PSPAPSDAAGMPKFT 533

Qy  545 ILKGIAAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRFN-EDGTEKSDFVLNKEP 603
        .|:| ||||: ||||||.||||||||||||||||.|||::.||: : :||.: |:|||:||
Db  534 TLRGYAAPLDIANVDTDMIIPKQFLKTIKRTGLGTALFYNIRFDQATGEENPDFVLNQEP 593

Qy  604 YRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSFADIFFNNSFKNGMLPIPIKD 663
        ||::.|||||| |||||||||||||||:||||||:||||||||||||.||||||||.: |
Db  594 YRQSRILVCTGPNFGCGSSREHAPWAFNDFGIRSIIAPSFADIFFNNCFKNGMLPITL-P 652

Qy  664 QAQIEAIAAEAARAGKEIEVDLPNQLIKNATGETICTFEVEEFRKHCLVNGLDDIGLTMQM 723
        |.::|.:|||:|::.|:||||| ||:: :. |||  .||:||||||||||||||||||||:
Db  653 QDKVEMLAEHAKQKAELEVDLVNQVVRYPGGEV--PFDVEPFRKHCLVNGLDDIGLTMQK 710

Qy  724 EDKIAEFEAKMTRETPWLDGTGYLKRKGQGGKLAAKAVPVPTTNRGEEKKEPLEW 778
        .|:||||||| | .|||||| . |:.|..||||.:|..|.| .:.   |:|:|:|
Db  711 ADLIEAFEAKRSQTWPWLDGKDY------AGK-ATKFTPVATNT--AKKQKLDW 755


RESULT 2
LEU2_RHINI
ID   LEU2_RHINI    STANDARD;    PRT;    750 AA.
AC   P55811;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
DE   isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEU1.
OS   Rhizopus niveus.
OC   Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC   Rhizopus.
OX   NCBI_TaxID=4844;
RN   [1]
```

```
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
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LEU2_RHIPU
ID   LEU2_RHIPU    STANDARD;    PRT;    755 AA.
AC   P55251;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
DE   isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUA.
OS   Rhizomucor pusillus.
OC   Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC   Rhizomucor.
OX   NCBI_TaxID=4840;
RN   [1]
```

```
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
```

```
DR   EMBL; D67033; BAA11052.1; -.
DR   InterPro; IPR000573; Aconitase_C.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   InterPro; IPR004431; LeuD.
DR   Pfam; PF00330; aconitase; 1.
DR   Pfam; PF00694; Aconitase_C; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   TIGRFAMs; TIGR00171; leuD; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT   METAL       353    353    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       413    413    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       416    416    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   755 AA;  82486 MW;  4E40537136BA6D11 CRC64;
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Query Match             66.2%;
Best Local Similarity   68.0%;           Score 2682.5;  DB No. 1.3e-173;  DB 1;  Length 755;
Matches  527;  Conservative  77;  Mismatches 144;  Indels 27;  Gaps 12;   Pred. No. 1.3e-173;

Qy    9 QTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD 68
        :||||||  : |||:|||:|||||||||||||||||||||||||||||||||:||| |
Db    3 RTLYDKVWDDHVDQQEDGTCLIYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCLATVD 62

Qy   69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG 128
        ||:|||.||: |::.:||:|:||||||:.|||:||||||:||| .|.||||||||||||||
Db   63 HNIPTTPRKNFKNVSTFIQEADSRTQCETLEHNVKEFGLTYFGMDDSRQGIVHVIGPEQG 122

Qy  129 FTLPGTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
        |||||. |.:||||||||||||||:||||||||||||||| |:.::|:||  |||:|||
Db  123 FTLPGCTVNCGDSHTSTHGAFGALAAFGIGTSEVEHVLATQTLLQKKSKNMVKVDGKLAP 182
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DR   EMBL; D63833; BAA09893.1; -.
DR   InterPro; IPR000573; Aconitase_C.
DR   InterPro; IPR001030; Aconitase.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   InterPro; IPR004431; LeuD.
DR   Pfam; PF00330; aconitase; 1.
DR   Pfam; PF00694; aconitase_C; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   TIGRFAMs; TIGR00171; leuD; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT   METAL   353   353   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL   413   413   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL   416   416   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   750 AA;   81308 MW;   7D7BE28304E26AB3 CRC64;
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Query Match             62.8%;  Score 2546;  DB 1;  Length 750;
Best Local Similarity   63.5%;  Pred. No. 2.2e-164;
Matches 502;  Conservative  90;  Mismatches 136;  Indels 62;  Gaps 12;
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Qy    9  QTLYDKVLQAHVVDEKLDGTYLVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD   68
            ||||||| |||..|.|:|:|||:||.|:||.|||||||||||||||||||||||||| .|.|
Db    3  RTLYDKVLEDHIIDRQEYGTCLIYIDRHLVHEVTSPQAFEGLRNAGRPVVRPDCTLATVD   62

Qy   69  HNVPTISRKALKDIASFIKEDDSRTQCVTLEENVKEGVTIYGLSDKRQGIVHVIGPEQG   128
            ||:||: ||.|||||.||||.||.|||.||.|:.|.| |.|::|::||||||||||||||
Db   63  HNIPTSPRNFKDIATFIKEGDSSTQCETLGENIEAFGLTYFGMEDSRQGIVHVIGPEQG   122

Qy  129  FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP   188
            ||||||||||||||||||||||||||||||||||||||||.|:.|||||||||:..|.:|
Db  123  FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQTLLQKKSKNMRIVEGKPSA   182

Qy  189  GVSSKDVVLHAIGIIGITGAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD   248
            ||:|||. |.||:||:.|||||| |||||||.|.|:||ME:|||||||||||.||||||:|||
Db  183  GVTSKDIALHVIGVIGTAGGTGCVIEFCGEANESLSMESRMSICNMSIEAGARAGMIAPD   242

Qy  249  EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAXKYDIDVFIDAKDIVPTLITWGTSP   308
            :ITFEYL ..PLA.K  ||..||  || |||  |..||:||:|.|: |||.||:|:|||||
Db  243  DITFEYLCNKPLASK--GEEWDRAVAVWKTLKFDADAQYDITVDIKASDIAPIVTWGTSP   300

Qy  309  EDVVPITGVVDPETFATEAKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIED   368
            :||.||||  ||:.||:.||.:|||:|.||.::. | ||:| |||||||||||||||:|
Db  301  QDVAPITGKTPDLDSIADPLRRLAVQRALDYIGIASNTPLEGVKIDKVFIGSCTNSRIED   360

Qy  369  LRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGM   428
            | .|||:|||.:.|:.|  .||||||.||||:||..:|||||||||||.||||||||||||
Db  361  LGPAAAIVKGKRVADWV--DAMVVPGSALVKRQAERKGLDKIFQEAGFNWREAGCSMCLGM   419

Qy  429  NPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL-------   480
            |||:| |:||||||||||:|||||||||||:.||.||||||||. |:|||:..:.||.|:
Db  420  NPDQLKPGERCASTSNRNFKGRQGAGGRTHLLLSPAMAAAAGICKCLTDVRHMEVAGIALT   479

Qy  481  -----TDYKASPHIAAYQKSTVTKPHVDERINQDAHEKDIIADIPEDNNGPHTN   529
             :::. | :|:|::||.|:|.: .||.|...:.. ..:.|  ||.:.:.||:
Db  480  GNESPRQEVVASRYDGSPEV--FKSTQDTTPAVKP--------PQ--; PASD   518

Qy  530  TSASVGTSAGLPKPTILKGIAAPLEKANVDTDAIIPKQFLKTIIKRTLGNALFYEMRFN   588
            :|:||| |||:||.|:|||:||||::.|.|||:|||||||||||||||||:||||.:|:.
Db  519  SS----SSGGMPAFTTLKGYAAPLDISNDTDMIIPKQFLKTIIKRTLGSALFYSLRFDP   574

Qy  589  EDGTEKSDFVLNKEPYRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSFADIFF   648
            :|| | ...||.||..||||||||||:|||||||||||||||.|||||.|||||||||||
Db  575  QTGAENPAFVLKERTFRQARILVCTGENFGCGSSREHAPWAFNDFGIRCILAPSFADIFF   634

Qy  649  NNSFKNGMLPIPIKDQAQIEAIAAEARAGKEIEVDLPNQLIKNATGETICTFEVEERKH   708
            ||.|||||||| :.|:||:||| ||.|.:|.|||||: |::: |..||:  :||||||||
Db  635  NNCFKNGMLPI-VLPQAQLEAIRAEBAQXGVEVEVDLVQQIVRNPGGEV--SPDVEEFRKH   691

Qy  709  CLVNGLDDIGLITWQMEDKIAEFFAKMTRETPWLDGTGYLKRKGCQGGKLAAKAVPVPTINR   768
            ||||||||||||||||:||:||||::| |:||||||:|||  | :|||||||:|.   |:|
Db  692  CLVNGLDDIGLITWQKADRIAQFETKRTQTWPWLDGKGY---KGKATKI---------EING   740

Qy  769  GEEKKEPLEW   778
            |:| | |:|
Db  741  GQQKKAKLDW   750
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RESULT 3

```
ID   LEU2_PHYBL     STANDARD;     PRT;    744 AA.
AC   P12250;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
DE   isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEU1.
OS   Phycomyces blakesleeanus.
OC   Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC   Phycomyces.
OX   NCBI_TaxID=4837;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90356419; PubMed=2388845;
RA   Iturriaga E.A., Diaz-Minguez J.M., Benito E.P., Alvarez M.I.,
RA   Eslava A.P.;
RT   "Nucleotide sequence of the Phycomyces blakesleeanus leu1 gene.";
RL   Nucleic Acids Res. 18:4612-4612(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92224296; PubMed=1563047;
RA   Iturriaga E.A., Diaz-Minguez J.M., Benito E.P., Alvarez M.I.,
RA   Eslava A.P.;
RT   "Heterologous transformation of Mucor circinelloides with the
RT   Phycomyces blakesleeanus leu1 gene.";
RL   Curr. Genet. 21:215-223(1992).
RN   [3]
RP   IDENTIFICATION OF PROBABLE FRAMESHIFT.
RA   Gibson T.J.;
RL   Unpublished observations (MAR-1996).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Monomer.
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC   -!- CAUTION: Ref.1 and Ref.2 sequences differ from that shown due to a
CC       frameshift in position 676.
CC   -----------------------------------------------------------------------
```

```
DR   EMBL; X53080; CAA37257.1; ALT_FRAME.
DR   PIR; S10998; S10998.
DR   PIR; S26864; S26864.
```

Mon Mar 17 09:02:05 2003

```
RESULT 4
LEU2_USTMA
ID   LEU2_USTMA     STANDARD;     PRT;     773 AA.
AC   P49601;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
DE   isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEU1.
OS   Ustilago maydis (Smut fungus).
OC   Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC   Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX   NCBI_TaxID=5270;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94171070; PubMed=8125330;
RA   Rubin B.P., Li D., Holloman W.K.;
RT   "The LEU1 gene of Ustilago maydis.";
RL   Gene 140:131-135(1994).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L20832; AAA34226.1; -.
DR   InterPro; IPR000573; Aconitase_C.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   InterPro; IPR004431; LeuD.
DR   Pfam; PF00330; aconitase; 1.
DR   Pfam; PF00694; Aconitase_C; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   TIGRFAMs; TIGR00171; leuD; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT   METAL     355    355    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL     415    415    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL     418    418    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   773 AA;  83224 MW;  A936D8D1990DDC1C CRC64;
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Query Match             61.5%;  Score 2492.5;  DB 1;  Length 773;
Best Local Similarity   64.0%;  Pred. No. 9.4e-161;
Matches  488;  Conservative  92;  Mismatches 142;  Indels  41;  Gaps  9;

Qy      8 PQTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATT 67
            |:|||||| | ||| ||||||||:||||||||||||||||||||||| :|||| ||||
Db      3 PKTLYEKIFDSHLVHEEADGTCLIYIDRHLVHEVTSPQAFEGLRNANRKVRRTDCTLATV 62

Qy     68 DHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQ 127
            ||| ||:||:|| :| || :::  ::| : |||||||:||:|||||:||:|||||||||
Db     63 DHNIPTASRKSYRDTKSFVEQVDSRTQCMTLEENVKAFGLTFFGLSDNRQGIVHIIGPEQ 122

Qy    128 GFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELA 187
            |||||||||| ||||||||||||||||||||||||||||||||||:|||||||||:|| :
Db    128 KATKVTAIGSASQPAKKLDW 744
```

```
DR   InterPro; IPR000573; Aconitase_C.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   InterPro; IPR004431; LeuD.
DR   Pfam; PF00330; aconitase; 1.
DR   Pfam; PF00694; Aconitase_C; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_C; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   TIGRFAMs; TIGR00171; leuD; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT   METAL     341    341    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL     401    401    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL     404    404    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   744 AA;  80833 MW;  9E5A930891D3745C CRC64;
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Query Match             62.7%;  Score 2543;  DB 1;  Length 744;
Best Local Similarity   66.1%;  Pred. No. 3.4e-164;
Matches  511;  Conservative  68;  Mismatches 160;  Indels  34;  Gaps  11;

Qy      9 QTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD 68
            |||||| | |            |||||||||||||||||||||||| :|||| ||||
Db      3 RTLYDKVWDDHV-------IDRHLVHEVTSPQAFEGLRNASRVRRPDCTLATVD 50

Qy     69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG 128
            |:||||:||:||:  | |||: : | :  ||| ||:||:|||||:||:|||||||||||
Db     51 HNIPTTTRKKFKSITTFIDEADSRTQCETLETNVKEFELTYFGMEDSRQGIVHVIGPEQG 110

Qy    129 FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
            ||||||||||||||||||||||||||||||||||||||||||:|||||||||| | ::
Db    111 FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRVCVEGELTP 170

Qy    189 GVSSKDVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD 248
            |:||||  |||||:||||||||: : |||| ||||:|||||||||||||||||||:|||
Db    171 GVTSKDVALHVIGLIGTAGGTRCVIEFCGSAIASLSMEARMSICNMSIEGGARAGMIAPD 230

Qy    249 EITFEYLRGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP 308
            ||||||||||| :| :      |::|  |||:   |||| ::| |:|| ||| :||||||
Db    231 EITFEYLRGRPLAP--EGAEWDKAVQYWKSLKSDPNAKYDIDVKIAASDIAPTITWGTSP 288

Qy    309 EDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIED 368
            :|||| |   | |:|| :|::| |         |||   ||:||:| |  ||||||||||
Db    289 QDVAPITANVPDPSSVSDPARKAAMERALEYIGLVPNTPLEEVKIDKAFIGSCTNSRIED 348

Qy    369 LRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGM 428
            ||:||  :|| ::|  |:  :| |||||||:|||:|| ||::| ||| ||||| ||||||
Db    349 LRSAASIVKGKHIADWV-YAMVVPGSGLVKRQAEREGLDKVFTDAGFDWREAGCSMCLGM 407

Qy    429 NPDILAPQERCASTSNRNFEGRQAGGRTHLMSPVMAAAAGIVGKLADVRKLTDYKASPH 488
            |||:|  :||||||||||||||||||||||||| ||||   |: | |:||: |||||:
Db    408 NPDQLSPGERCASTSNRNFEGRQAGGRTHLMSPAMARAAAAIRGYLTDVRKFSSTPMVPR 467

Qy    489 IAAYQKSTVTKPHVDERI--NQDAHEKDIIADIPEDNNGPHTNTSASVGTSAGLPKFTIL 546
            :|| |||:|||  | |||   ||| |: | ||:||::|||| ||:|| |:|||||||| |
Db    468 SPPPKFQTI-QPKVEDEAAHKQAADQADPVTDCPP--AGSPVNKGAPV--ASAMPAFTTL 522

Qy    547 KGIAAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRFN-EDGTEKSDFVLNKEPYR 605
            ||:|||| |||  ||:||||||||||||||||:||||:||| |  :|||:||:|| |||
Db    523 KGVAAPLAISNVDTDMIIPKQFLKTIKRTGLGSALFYGLRYDPATGAEKPDFVLNQPAYR 582

Qy    606 KASILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSFADIFFNNSFKNGMLPIPIKDQA 665
            :|||||||| | |||||||||||| |||||||:|:|||||||||||:|||||||||:|||
Db    583 SSKILVCTGPNFGCGSSREHAPWANFNDFGIRCIIATSFADIFFNNCFKNGMLPI-ILSQE 641

Qy    666 QIEAIAAEARAGKEIEVDLPNQLIKNATGETICTFEVEEFRKHCLVNGLDDIGLTMQMED 725
            ||  || |:|| ||||||||:| |||||| | ||||||:||| ||:||||||||||||:|
Db    642 QVDTLAKYATQKAEIEVDLVHQKIRYPGGEIPFDXMIEEFRKHCLVNGLDDIGLTMQKDS 701

Qy    726 KIAEFEAKMTRETPWLDGTGYLRKGQGGKLAAKAVPVPTTNRGEEKKEPLEW 778
            ||:|||| |||:|||||||||||:|  || |||:|||||||||:|||||| |
Db    702 AIEKFEAKRTSTWPWLDGKAY------KG------KATKVTAIGSASQPAKKLDW 744
```

```
Db   123 GFTLPGATIVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQTLLQKRAKNMLIQVDGELS 182
                                                                       
Qy   188 PGVSSKDVVLHAIGIIGITGAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAP 247
         |::|:|     | |||||::::|   :| ||||:||::::|:| ||:|| ||:::: |
Db   183 QGVTSKDILHIGLGITAGGTGHVLEYAGSTIRSLSMEARMSICNMSIEAGARAGLIAP 242

Qy   248 DEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTS 307
         |:|||:|||||| ||  |::|||:||:|||||| :||||||:||||||||||||||||
Db   243 DEITYEYIKGRPLAPK-QGEAWDQALLAYWKTLPSDEGAQYDTVIKIDAKDIPPTVTWGTS 301

Qy   308 PEDVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTTNSRIE 367
         ||::|:|| ||:|::|||:|||:| |:|||||:||||||| ||:||||||||||:|||:
Db   302 PQDVVAITGTVPDPKNASNEABAKAWTRALEYMGLEAGTPMEKIKIDKVFIGSCTNARIE 361

Qy   368 DLRAAAAVKGRKKAPNVKSAMVVPGSGLVKTQAEEBGLDKIFERAGFEWRBAGCSMCLG 427
         ||||||:|||  |   :| ::| |||||: |||:| :|:|||||:|| ||::|||:|||
Db   362 DLRAAARVLHGRKVADGL-YCMLVPGSGLVKQAEAEGLDKIFQAAGFDWREAGCCSMCLG 420

Qy   428 MNPDILAPQERCASSTSNRNFEGRQGAGGRTHLMSPVNAAAAGIVGKLADVRKLTDYXASP 487
         |:|| |||||||:| ::|::|  |||||| |:         |||||  |||: :||||||
Db   421 MNPDQLAPGERCASTSNRNFEGRQGAGGRTHLMSPAMAAACAVTGYLTDVRKVVG----- 475

Qy   488 HIAAYQKSTVKPHVDERINQ--------DA-------HEKDIADIPEDNN 524
         :: :                 :: |:|         :||:|||:|:|
Db   476 HSSAKVGSDAAKPAPEIEVSDAKSYLVDATPAPATNVAAGAGALTDEDALRDVP---- 531

Qy   525 GPHTNTSASVGTSAGLPKFTILKGIAAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYE 584
         |||||||| |||   ||||:||||:|||||:|:|||||::|||||||||||||| | |
Db   532 ASHISSS-----GGGMEKFTILTGIAAPLERSNVDTDLIIPKQFLKTIKRTCLGSALFWP 586

Qy   585 MRFN-EDGTEKSDFVLNKEPYRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSF 643
         ||   :|| ::||||| |:| ::|||:|||||||||||||||||| |:||||| :||||
Db   587 LRYDAKTGEPDPAFVLNQKPVDQSKILVVTGPNFGCGSSREHAAWSLLDFGIRAVIAESF 646

Qy   644 ADIFNNNSFKNGMLPIPKDQAQIEAIAAEARAGKEIEVDLPNQLIKNATGETICTFEVE 703
         |||| |::||| ||:||||| || :|||:|||||||||||:||||:||:|||||| ||
Db   647 GDIFRNNLTKNGQLPV-VLSRAQIQRLTQDAKAGKQITVDLVDQLVITADGKEKFSFETP 705

Qy   704 EFRKCLVNGLDDIGLTMQMEDKIAEFEAKMTRETPWLDGTGY 746
         || : |:|||||: ||:|:||:| | |:|::|  |||| ||
Db   706 EFTRHCLINGLDDIALTLQRDAQIGAFERNRSTHTPWLDGFGY 748
```

RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).

```
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC   -------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------
EMBL; Z992262; CAB16402.1; -.
InterPro; IPR000573; Aconitase_C.
InterPro; IPR001030; Aconitase.
InterPro; IPR001030; Aconitase_N.
InterPro; IPR004430; LeuC.
InterPro; IPR004431; LeuD.
Pfam; PF00330; aconitase; 1.
Pfam; PF00694; Aconitase_C; 1.
PRINTS; PR00415; ACONITASE.
ProDom; PD000511; Aconitase_N; 1.
PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_2; 1.
TIGRFAMs; TIGR00170; leuC; 1.
TIGRFAMs; TIGR00171; leuD; 1.
PROSITE; PS00450; Aconitase; 1.
PROSITE; PS01244; Aconitase_C.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT   METAL       359    359       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       420    420       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       423    423       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   758 AA;  82782 MW;  CE78C36E28380B47 CRC64;
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Query Match             61.0%;  Score 2473.5; DB 1;  Length 758;
Best Local Similarity   62.9%;  Pred. No. 1.8e-159;
Matches  489;  Conservative  92;  Mismatches 172;  Indels  25;  Gaps  9;
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```
Qy     1 MPGARSTPQTLYDKVLQAHVVDEKLDGTVLVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRP 60
                  :::|| :|||||  |  | |:|:|  ||||: ||:||:::|| |  :||
Db     1 MSPSVASPKTLYDKVWDSHVVDLQEDGTCLLYIDRHLIHEVTSPQAFEGLRTAGRKVRHP 60

Qy    61 DCTLATTTDHNVPTTISRKALKDIASFIKEDDSRIQCCVTLEENVKEFGVTIFGLSDKRQGIV 120
         |:  :| : |  ||  :    |: |:||:   ::| :   :||||:||||:|| |:||:||||
Db    61 ELALATVDHNIPTDPRKDMKDIASFIHQPDSRTQVLALENNIKEFGLTYGMNDRRQGIV 120

Qy   121 HVIGPEQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRI 180
         |||||||||||||| |||||||||||||||||||||||||||||||::|:||||||||:|
Db   121 HVIGPEQGFTLPGITVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQTLLQRKSKNMRI 180

Qy   181 QVDGELAPGVSSKDVVLHAIGIIGITGAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGA 240
         |:|:| :: |  ||:||| |||||||  |||||||||||||||||||||||||||||||||
Db   181 RVNGLKLPEGIASKDILIHIIGVIGITAGGTGSVIEFCGEAIEGLSMEARMSMCNMSIEAGA 240

Qy   241 RAGMVAPDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVP 300
         ||| :|||  | ||||||| ||   ||||||||| |||  || |  | | | : ||  :|
```

```
RT    "The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1
RT    and ATE1 loci on chromosome VII from Saccharomyces cerevisiae reveals
RT    the PDR6 gene, a new member of the genetic network controlling
RL    pleiotropic drug resistance.";
RL    Yeast 7:287-299(1991).
CC    -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC        and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC    -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC        H(2)O.
CC    -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC        isopropylmalate.
CC    -!- PATHWAY: Leucine biosynthesis; second step.
CC    -!- SUBUNIT: Monomer.
CC    -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC    --------------------------------------------------------------------------
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CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; S57886; AAB19612.1; -.
DR    EMBL; Z72531; CAA96709.1; -.
DR    EMBL; K01969; AAA34742.1; -.
DR    EMBL; S58126; CAB31643.1; -.
DR    PIR; A24105; A24105.
DR    PIR; S15039; S15039.
DR    PIR; S31555; S31555.
DR    SGD; S0002977; LEU1.
DR    InterPro; IPR000573; Aconitase_C.
DR    InterPro; IPR001030; Aconitase_N.
DR    InterPro; IPR004430; LeuC.
DR    InterPro; IPR004431; LeuD.
DR    Pfam; PF00330; aconitase; 1.
DR    Pfam; PF00694; Aconitase_C; 1.
DR    PRINTS; PR00415; ACONITASE.
DR    ProDom; PD000511; Aconitase_N; 1.
DR    TIGRFAMs; TIGR00170; leuC; 1.
DR    TIGRFAMs; TIGR00171; leuD; 1.
DR    PROSITE; PS00450; ACONITASE_1; 1.
DR    PROSITE; PS01244; ACONITASE_2; 1.
KW    Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT    METAL       360    360       IRON-SULFUR (4FE-4S)   (BY SIMILARITY).
FT    METAL       421    421       IRON-SULFUR (4FE-4S)   (BY SIMILARITY).
FT    METAL       424    424       IRON-SULFUR (4FE-4S)   (BY SIMILARITY).
FT    CONFLICT    291    291       N -> TLKH (IN REF. 1).
FT    CONFLICT    423    423       I -> M (IN REF. 1).
FT    CONFLICT    459    459       M -> I (IN REF. 1).
FT    CONFLICT    744    744       R -> K (IN REF. 1 AND 4).
SQ    SEQUENCE   779 AA;  85794 MW;  BD409A9702AE3E57 CRC64;

Query Match             60.6%;  Score 2456.5;  DB 1;  Length 779;
Best Local Similarity   63.1%;  Pred. No. 2.6e-158;
Matches  486;  Conservative  93;  Mismatches 152;  Indels  39;  Gaps  10;

Qy      8 PQTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATT 67
          |  ||| ||| ||||  |:|  |:|||:||||||||||||| ||||:|||| || ||||
Db      9 PRTLYDKVFDAHVVHQDENGSFLLYIDRHLVHEVTSPQAFEGLENAGRKVRRVDCTLATV 68

Qy     68 DHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQ 127
          |||:||| || ||| ||:|| |||:||  |:|||||  |||||||  |:| | |||:| :
Db     69 DHNIPTESRKNFKSLDTFIKQTDSRLQVKTLENNVKQFGVPYFGMSDARQGIVHTIGPEE 128

Qy    128 GFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVHVLATQCLITKRSKNMRIQVDGELA 187
          ||||||||||||||||||||| || ||| |||||||| |: | |||||||:| : :: :
Db    129 GFTLPGTTVVCGDSHTSTHGAFGSLAFGIGTSEVHVLATQTIIQAKSKNMRITVNGKLS 188

Qy    188 PGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAP 247
          || :||:|:|  ||||||:|||| |||| |  : |||||||||| || | :| ||||  |
Db    189 PGITSKDLILYIGLIGTAGGTGCVIEFAGEAIEALSMEARMSMCNMAIEAGARAGMIKP 248
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RESULT 6
LEU2_YEAST
ID   LEU2_YEAST     STANDARD;      PRT;    779 AA.
AC   P07264;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
DE   isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEU1 OR YGL009C.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Il125-2B;
RX   MEDLINE=91353082; PubMed=1840714;
RA   Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;
RT   "Complete sequence of the Saccharomyces cerevisiae LEU1 gene encoding
RT   isopropylmalate isomerase.";
RL   Yeast 7:281-285(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RP   SEQUENCE OF 1-48 FROM N.A.
RA   Hebling U., Hofmann B., Delius H.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 1-48 FROM N.A.
RX   MEDLINE=84162042; PubMed=6323436;
RA   Hsu Y.-P., Schimmel P.R.;
RT   "Yeast LEU1. Repression of mRNA levels by leucine and relationship of
RT   5'-noncoding region to that of LEU2.";
RL   J. Biol. Chem. 259:3714-3719(1984).
RN   [4]
RP   SEQUENCE OF 740-779 FROM N.A.
RC   STRAIN=Il125-2B;
RX   MEDLINE=91353083; PubMed=1882553;
RA   Chen W., Balzi E., Capieaux E., Choder M., Goffeau A.;
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Db    241 RAGMIAPDATTFEYVKNRPLAPKGD--DWEQAVAYWKTLRSDENAKYDIEVEINAADVLP 298
          ||||||||||||||||||||||||   :|||||| ||||||||||| |||| ||||| ||
Qy    301 TLTWGTSPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGS 360
          | || | | ||||:| ||| ||  :  |   ||:||| |||||| ||||||||||||||
Db    299 TVTWGTSPQDVVPINGNIPDPAHVKDNVRAASIQRSLEYMGLKPNTSIVSYPIDKVFIGS 358

Qy    361 CTNSRIEDLRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREA 420
          ||||||||||||||||||||| |||||| |||||||:||| |::||||| ||||| |||
Db    359 CTNSRIEDLRLAAAVVKGRKVAAANVKDAMIVPGSGLVKKMAEAEGLDQIFIEAGFDWREA 418

Qy    421 GCSMCLGMNPDILAPQERCASTSNRNFEGROGAGGRTHLMSPVMAAAAGIVGKLADVRKL 480
          |||||||||||:| |||||||||||||||| |||| ||| ||:|| |  || |||  ::
Db    419 GCSMCLGMNPDQLKPYERCASTSNRNFEGROGAKGRTHLVSPAMAAAAAIKGHLCNVREF 478

Qy    481 TDYKASPHIAAYQKSTVTKPHVDERINQDAH---EKDIIADIPEDNNGPHTNTSASVGT- 536
          ||   |   ::  :||||| |    || ||      :| :|| ||    |:|:|||| ||
Db    479 FG-----DVSNGSPIITNKNYDPSHDVEGDIGLSVDDATDAVTDADGIATNVAGSVSSG 533

Qy    537 SAGLPKFTILKGIAAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRFNEDGTEKSD 596
          |||:||| ||||||||:||||||||||||||||||||||||||| ||:|| |: ||:|||
Db    534 SAGIPKFTTVEGIAAPLPMANVDTDKIIPKQFLKTIKRTGLGQFAFYEIRYDADGKEIPD 593

Qy    597 FVLNKEPYRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSFADIFFNNSFKNGM 656
          |||| ||||:  :||| :| ||||||||||||||||||||:||||||||||||| |:|||
Db    594 FVLNREPYRHATVLVAHD-NFGCGSSREHAPWALNDFGIRVIIAPSFADIFFNNCFKNGM 652

Qy    657 LPIPIKDQAQIEATAAEARAGKEIEVDLPNQLIKNATGETICTFEVEEFRKHCLVNGLDD 716
          |||  :|| || :   |:||||:|    :  :|| | ||:||  |:|||||||| ||||
Db    653 LPIPTPIE-QVNDMMKAAENQVKFSVDLVNQTI--TYGDKQVKFDVEPFRKHCLVNGLDD 709

Qy    717 IGLTMQMEDKIABFFAKMTRETPWLDGTGYLKRKGQGGGKLAAKAVPVPTTNRGEEKKE 774
          ||||  |:|| |  |:|:   :||  ||  |  ||       :|| :||||:| |::|
Db    710 IGLTLQKETMIDAFEAARENFPWMN----IKRS------RARLSPVKSNKQSSSRND 757
```

```
RESULT 7
ID   LEU2_CANMA     STANDARD;      PRT;   770 AA.
AC   Q00464;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
DE   isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEU1.
OS   Candida maltosa (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5479;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=L4;
RA   Becher D., Jomantiene R., Schulze S., Bode R., Oliver S.G.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- PATHWAY: Leucine biosynthesis (By similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC   -----------------------------------------------------------------
DR   EMBL; U60167; AAB03335.1; -.
DR   InterPro; IPR000573; Aconitase_C.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   InterPro; IPR004431; LeuD.
DR   Pfam; PF00330; aconitase; 1.
DR   Pfam; PF00694; Aconitase_C; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   TIGRFAMs; TIGR00171; leuD; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT   METAL       354    354    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       415    415    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       418    418    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   770 AA;  85317 MW;  CB1C26A56D7C3C1A CRC64;
```

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Query Match             59.6%;  Score 2417.5;  DB 1;  Length 770;
Best Local Similarity   61.9%;  Pred. No. 1.1e-155;
Matches  491;  Conservative  79;  Mismatches  178;  Indels  45;  Gaps  12;
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Qy   7 TPQTLYDKVLQAHVDERKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLAT 66
         |||||||| | ||::|:|| | *||||||||||||||||||||||:||||.|||.||||||
Db   2 SPKTLYDKVFEDHIIVEDESGSNLLYIDRHLVHEVTSPQAFEGLKNAGRTVRRTDCTLAT 61

Qy  67 TDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPE 126
         |||:|| ||  .| :|: :|:||||| |: ||| ||::| ||||| ||:||||||| ||
Db  62 VDHNIPTISRVNFKTLLITFIDQDDSRLQVQTLEQNVKDFDVTYFGMTDDRQGIVHVVGPE 121

Qy 127 QGFTLPGTTVVCGDSHSTHGARGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGEL 186
         |||||||||||||||| |||| ||||||||||||||||||| :|  :.||||||::||| 
Db 122 QGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQTTIQANPKNMRITIDGEL 181

Qy 187 APGVSSKDVVLHAIGIIGTTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVA 246
         : |:|||| |||.||:||||||||| |||| | .|. |||||||||||:|||||||||:  
Db 182 SEGITSKDLVLHVIGVIGVTTAGGTGCVIEFAGKAIEDLSMEARMSICNMAIEBAGARAGMIK 241

Qy 247 PDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPFLTWGT 306
         |||:||||:||||||||    || ||  ||:.| :| ||| | |:| :|.||||.|:|| 
Db 242 PDEKTFEYIKGRPLAPKGD--EWEKALYXWKTLHTDDGAKLHYDIKIAASDIVPTITWGN 299

Qy 307 SPEDVVPITGVVPDPETPATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRI 366
         || ||.|||.|||| ...  .|||:||| | :|:||  :||:  | ||||||||||||| 
Db 300 SPQDALPITASVPDPANVSDPIKKSGMERALKYQGLTPNTPFVVIKMHKAFIGSCTNSRI 359

Qy 367 EDLRAAAAVKRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCL 426
         ||||||| | :.|  ||  :||||||||:| |||:||||||||.||| |||||||||| 
Db 360 EDLRAAAKVAKGHKKADNVKLVLVVPGSGLIKKQAEKEGLDKIFESAGFTWREAGCSMCL 419

Qy 427 GMNPDILAPQEBRCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKLTDYKAS 486
         |||||||.|.| ||||||||||||||||   ||||||.||||| ||:  :| |  : |:  
Db 420 GMNPDILDPEERCASTSNRNFEGRQGARSRTHLMSPAMAAAAIKGHFTDIREF-DYVDN 478

Qy 487 PHIAAYQKSTVTKPH-VDERINQDA---HEKDIIADIPEDNNGPHTNTSASVGTISAGLPK 542
         .   |::.  .|:.| ||:| :|:|   |||:||  | |:  .  |..| ||| :|||||  
Db 479 -----DEPSITIEHEVEDKELQDAVEHEKEIIEGTP-GTEAERSTTSLKMNQNSKKPN 531

Qy 543 FTILK--------------GIAAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRFNEDG 591
         ::|:|              |||||| |||||||||||||||||||||||.| ||||.||.  
Db 532 QMLIKMVPITVLPFLIGITIAPLYKANVDTDAIIPKQFLKTIKRTGLKNGLFYESRFVKMP 591

Qy 592 TEK--SDFVLNKEPYRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSFADIFN 649
         |    :|||||:||||:|.||| ||:||||||||||||||:|||||||:||||| ||| 
Db 592 MVRCQTDFVLNVEPYRQAEILVTGDNFGCGSSREHAPWALKDFGIKSIIAPSFGDIFYN 651

Qy 650 NSFKNGMLPIPIKDQAQIEAIAAEARAGKEIEVDLPNQLIKNATGET-----ICTFEVEEF 705
         |||||.||||||:.| :| :: :  .  |:  | ||||| |:| |:|     || ||||| 
Db 652 NSFKNFLLPIRIPQDVIESKLVPVVKAGHKLTITDLPNQQIKD--GETGDVLIEKFDVEEF 709

Qy 706 RKHCLVNGLDDIGLTMQMEDKIAEFEAKMTRETPWLDGTGYLKRKGQGGKLAAKAVPVPT 765
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Db    710 RKHCLVNGLDDIGLTLQKEYIQEYEAKRREKFSFLEG-------GSKLIK---PIKG 757
              ||||||||||||||||||  |: |:||  :|:|                    ||  |:
Qy    766 TNRGEEKKEPLEW 778

Db    758 TKKSIYGNKAQEW 770
```

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RESULT 8
LEU2_RHIRA
ID   LEU2_RHIRA    STANDARD;       PRT;   644 AA.
AC   P17279;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
DE   isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUA.
OS   Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
OC   Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC   Mucor.
OX   NCBI_TaxID=4841;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 1216B;
RX   MEDLINE=90128278; PubMed=2693214;
RA   Isabel M., Roncero G., Jepsen L.P., Stroeman P., van Heeswijck R.;
RT   "Characterization of a leuA gene and an ARS element from Mucor
RT   circinelloides.";
RL   Gene 84:335-343(1989).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Monomer.
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC   --------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; M33166; AAA33422.1; -.
DR   PIR; JQ0160; JQ0160.
DR   PIR; S26865; S26865.
DR   InterPro; IPR000573; Aconitase_C.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   Pfam; PF06694; Aconitase_C; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT   METAL       400    400       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       460    460       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       463    463       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   644 AA;  69939 MW;  087FC2C518BD497E CRC64;

Query Match       51.2%;  Score 2076;  DB 1;  Length 644;
Best Local Similarity 68.8%;  Pred. No. 9.9e-133;
Matches 407;  Conservative 60;  Mismatches 111;  Indels 14;  Gaps 6;

Qy     10 TLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTDH 69
              |||||  ||:::  ||| ||||||||||||||||||||| | ||||||| |||||||||
Db     51 TLYDKVWDDHVIDQQEDGTCLIYIDRHLVHEVTSPQAFEGLRNANRPVRRPDCTLATVDH 110
```

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Db     70 NVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQGF 129
              |:||:|||||:| |: |::|||||:|||||||||||||:||||:|:|||||||||||||
Qy     70 NIPTTTRKIFKNITTFIKEADSRTQCETLEQNIEAFGLTYFGMEDSRQGIVHVIGPEQGF 170
```

Db   111 NIPTTTRKIFKNITTFIKEADSRTQCETLEQNIEAFGLTYFGMEDSRQGIVHVIGPEQGF 170

```
Qy    130 TLPGTTVVCGDSHTSTHGFAGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAPG 189
              |||||||||||||||||||||||||||||||||||||||||||||:|||:||||||| ||
Db    171 TLPATTVVCGDSHTSTHGFAGALAFGIGTSEVEHVLATQTLLQKKSKNMRIRVQGKALPG 230
```

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Qy    190 VSSKDVVLHAIGIGTAGGTGAVIEFCCGSVIRSLSMEARMSICNMSIEGGARAGMVAPDE 249
              |:|||:|| |::|:|||||||||||||||||||:||||:|||||||||:|||||||||||
Db    231 VTSKDIVLHIIGVIGTAGGTGCVIEFCGDTIALSMESRMSICNMSIEARAGRAGMVAPDE 290
```

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Qy    250 ITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSPE 309
              :|||||| || || |||   || | ::|:|| :   |||  |||| ||:||||||||||
Db    291 VTFEYLRDKPLAPK--GADWDRAVKVWKSLSSDDADAKYDINVEINAADIAPTLTWGTSPQ 348
```

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Qy    310 DVVPITGVVPDPETFEATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIEDL 369
              ||||||| ||:|||||||||||||:|||| :  ::     ||| |||||||||||||||||
Db    349 DVVPITGSTPDFAKIEDFIRRSAVQRALDYIGIAPNTPMEGVKVDKVFIGSCTNSRIEDL 408
```

```
Qy    370 RAAAAVKGRKKAPNVKSAMVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGMN 429
              |||||||:  |||||||||:|||||||| |||||||||||:||||||||||||||||||
Db    409 RAAAAVKGKRAAEWV-DAMVVPGSGLVKRQAEREGLDKIFTDAGFDWREAGCSMCLGMN 467
```

```
Qy    430 PDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKLTDYKASPHI 489
              ||::|| |||||||||||||||||||||||:||:  :::|:||| ||:|::|||||||||::
Db    468 PDQLKPGERCASTSNRNFEGRQGAGGRTHLVSPAMAAAAGIKGCLTDVRNM------EV 520
```

```
Qy    490 AAYQKSTVTKPHVDERINQDAHEKDIIADIPEDNNGPHTNTSASVGTSAGLPKFTTLKGI 549
              :   :||| :  |: ::  :|  ||::||  |  :    |:::||:   |:|:||||||:||
Db    521 SEIPGTPKQSPRQEVVAEFESEEDDV--DSSSVDSAP-VATPPSTGDSAGMPKFTTLKGY 577
```

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Qy    550 AAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRFN-EDGTEKSDFVLN 600
              ||||:  :||:||||:||||||||||||||||:|:|:  :  |:|  ||||||
Db    578 AAPLDISNVDTDMIIPKQFLKTIKRTGLGSALFYALRFDPDATGAENPDFVLN 629
```

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RESULT 9
LEU2_RHIME
ID   LEU2_RHIME    STANDARD;       PRT;   469 AA.
AC   Q92L76; Q9EV53;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR R03206 OR SMC03823.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=21396507; PubMed=11481430;
RA   Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA   Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA   Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA   Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA   Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT   "Analysis of the chromosome sequence of the legume symbiont
RT   Sinorhizobium meliloti strain 1021.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
RN   [2]
RP   SEQUENCE OF 22-469 FROM N.A.
RC   STRAIN=GR4;
RA   Sanjuan-Pinilla J.M., Munoz S., Olivares J., Sanjuan J.;
RT   "The Sinorhizobium meliloti leuA gene is essential for symbiosis.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
```

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CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC       SUBFAMILY.
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DR   EMBL; AL591793; CAC47785.1; -.
DR   EMBL; AJ296268; CAC14578.1; -.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   METAL       350    350    IRON-SULFUR (4FE-4S)  (BY SIMILARITY).
FT   METAL       410    410    IRON-SULFUR (4FE-4S)  (BY SIMILARITY).
FT   METAL       413    413    IRON-SULFUR (4FE-4S)  (BY SIMILARITY).
FT   CONFLICT     31     31    R -> C  (IN REF. 2).
FT   CONFLICT     96     96    F -> V  (IN REF. 2).
FT   CONFLICT    270    270    T -> M  (IN REF. 2).
FT   CONFLICT    371    371    A -> S  (IN REF. 2).
SQ   SEQUENCE   469 AA;  50994 MW;  22A27D04064S726 CRC64;

Query Match             40.3%;  Score 1636;  DB 1;  Length 469;
Best Local Similarity   66.0%;  Pred. No. 3.4e-103;
Matches  313;  Conservative  57;  Mismatches  96;  Indels  8;  Gaps  3;

Qy      6 STPQTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLA 65
            |||||||| :||  ||: ||||||||||||||||||||||||  ||| ||  || | ||
Db      2 SAPRTLYDKIWDDHLVDSQDDGTCLLYIDRHLVHEVTSPQAFEGLHMAGRPVRHPEKTLA 61

Qy     66 TTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGP 125
            ..||||||||    |      ||   |||    | |  | ||| |  | :||||||| |||
Db     62 VVDHNVPTTSPDRHLG----IKNEESRIQVEALARNAADFGVEYYSENDKRQGIVHIVGP 116

Qy    126 EQGFTLPGTTVVCGDSHSTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGE 185
            ||||||||  :||||||||||||||||||  ||||||||||||| || |  ||| : | |:
Db    117 EQGFTLPGMTIVCGDSHSTSTHGAFGALAHGIGTSEVEHVLATQTLIQKKAKNMLVRVDGQ 176

Qy    186 LAPGVSSKDVVLHAIGIIGTAGGTGYVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMV 245
            | |||  ||   |  | ||||||||:|||| | :|||||||  | : ||| ||||||| |:
Db    177 LPPGVPAKDILAIIGEIGTAGGTGHVIEFAGEAIRSLSMEGRMTVCNMTIEGGARAGLI 236

Qy    246 APDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYIDIDVFIDAKDIVPTLTWG 305
            ||||:|||| |  | ||| :  :|  :  ||  |  :  |  ||| |  :||||| | :| |
Db    237 APDETTFEYIKDKPRAPKGEA----WDRAVEYWKTLHTDEGAHYDRVVVLDAANLPPIVSWG 294

Qy    306 TSPEDVVPITGVVPDPETFATEARKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSR 365
            :|||||  : |||| |: ::   :|    ||  | ||||| |  : | |  ||||||||| |
Db    295 SSPEDVVSVQGVVPNPDDIQDETKRTSKWRALDYMGLKPGTKITDIAIDRVFIGSCTNGR 354

Qy    366 IEDLRAAAAVKGRKKAPNVKSAMVPGSGLVKTQAEEGLDKIFEEAGFEWREAGCSMC 425
            ||||||   |  |:  |.  .|||||||||| ||| :|||||| |||:|||  ||||||
Db    355 IEDLRAVAEVGERKVAPTV-SAMVPGSGLVKEQAEAEGLDKIFKEAGFDWREPGCSMC 413

Qy    426 LGMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAGIVGKLLADVRK 479
            | :|  || | ||||||||||||||||   |||| || ||||   || |:|::|:
Db    414 LAMNDDLRKPGERCASTSNRNFEGRQGFKGRTHLLSPAMAAAAVAGHFVDIRE 467
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RESULT 10
LEU2_BRUME

ID   LEU2_BRUME     STANDARD;      PRT;   469 AA.
AC   Q8YCG9;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR BMEI0157.
OS   Brucella melitensis.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Brucellaceae; Brucella.
OX   NCBI_TaxID=29459;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=16M / ATCC 23456 / Biotype 1;
RX   MEDLINE=22020109; PubMed=11756688;
RA   DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA   Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA   Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA   Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA   Haselkorn R., Kyrpides N., Overbeek R.;
RT   "The genome sequence of the facultative intracellular pathogen
RT   Brucella melitensis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC       SUBFAMILY.
```

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DR   EMBL; AE009458; AAL51339.1; -.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   METAL       350    350    IRON-SULFUR (4FE-4S)  (BY SIMILARITY).
FT   METAL       410    410    IRON-SULFUR (4FE-4S)  (BY SIMILARITY).
FT   METAL       413    413    IRON-SULFUR (4FE-4S)  (BY SIMILARITY).
SQ   SEQUENCE   469 AA;  50692 MW;  14442D949C40BCDF CRC64;

Query Match             39.7%;  Score 1611;  DB 1;  Length 469;
Best Local Similarity   66.8%;  Pred. No. 1.6e-101;
Matches  316;  Conservative  51;  Mismatches  98;  Indels  8;  Gaps  3;

Qy      6 STPQTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLA 65
            |||||||| :||  ||: ||||||||||||||||||||||||  ||| ||  || | ||
Db      2 SAPRTLYDKIWDDHVVDQGEDGTCLLYIDRHLVHEVTSPQAFEGLHMAGRPVRHPEKTLA 61

Qy     66 TTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGP 125
            ..||||||:
Db     62 VVDHNVPTS-----PDRINQIQNEESRIQVEALARNAADFGVEYYSERDKRQGIVHIVGP 116

Qy    126 EQGFTLPGTTVVCGDSHSTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGE 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 EQGFTLPGTTVVCGDSHSTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGE 185
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Db        ||||||||   ||:||||||||||||||||||||||| ||||| ::  :||:|||
Qy  117 EQGFTLPGMTIVCGDSHTSTHGAFGALAHGIGTSEVEHVLATQTLIQKKAKNMLVRVDGK 176

Qy  186 LAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMV 245
Db  177 LPAGVTAKDIVLAIIGEIGTAGGTGVIEVAGEAIRSLSMEGRMTICNMSIEGGARAGLI 236

Qy  246 APDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWG 305
Db  237 APDETTFEYIKGRPRAPKGETLE--QAINYWKTLHSDEGAHFDKIVTLDAGSLPPIVSWG 294

Qy  306 TSPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSR 365
Db  295 SSPEDVVSVGVGVVPNPDDIADETKRASKWRALDYMGLKPGTKITDIAVDRVFIGSCTNGR 354

Qy  366 IEDLRAAAAVKGRKKAPNVKSAMVVPGSGLVKTQABEEGLDKIFEEAGFEWREAGCSMC 425
Db  355 IEDLRAAAKVVEGKKVAPTV-NAMIVPGSGLVKEQAEAEGLHKIFIEAGFPDWREPGCSMC 413

Qy  426 LGMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVR 478
Db  414 LAMNDDRLKPGERCASTSNRNFEGRQGFKGRTHLVSPAMAAAAAIAGHFVDIR 466

RESULT 11
LEU2_AGR5
ID  LEU2_AGR5    STANDARD;      PRT;    469 AA.
AC  Q8UBY9;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE  (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN  LEUC OR ATU2709 OR AGR_C_4910.
OS  Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC  Rhizobiaceae; Rhizobium.
OX  NCBI_TaxID=176299;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21608550; PubMed=11743193;
RA  Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA  Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA  Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA  Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA  Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA  Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA  Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA  Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA  Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA  Nester E.W.;
RT  "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT  C58.";
RL  Science 294:2317-2323 (2001).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21608551; PubMed=11743194;
RA  Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA  Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA  Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA  Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA  Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA  Cielo C., Slater S.;
RT  "Genome sequence of the plant pathogen and biotechnology agent
RT  Agrobacterium tumefaciens C58.";
RL  Science 294:2323-2328 (2001).
CC  -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC      and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC  -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC      H(2)O.
CC  -!- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC      isopropylmalate.
CC  -!- PATHWAY: Leucine biosynthesis; second step.
```

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CC  -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC  -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM_ISOMERASE FAMILY. LEUC 1
CC      SUBFAMILY.
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DR  EMBL; AE009217; AAL43690.1; -.
DR  EMBL; AE008184; AAK88428.1; ALT_INIT.
DR  InterPro; IPR001030; Aconitase_N.
DR  InterPro; IPR004430; LeuC.
DR  Pfam; PF00330; aconitase; 1.
DR  ProDom; PD000511; Aconitase_N; 1.
DR  TIGRFAMs; TIGR00170; leuC; 1.
DR  PROSITE; PS00450; ACONITASE_1; 1.
DR  PROSITE; PS01244; ACONITASE_2; 1.
KW  Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT  METAL       350    350    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT  METAL       410    410    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT  METAL       413    413    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ  SEQUENCE    469 AA;    51048 MW;    F8EFFE03DA610D39 CRC64;

Query Match             39.1%;  Score 1584;  DB 1;  Length 469;
Best Local Similarity   65.4%;  Pred. No. 1.1e-99;
Matches  310;  Conservative   52;  Mismatches  104;  Indels    8;  Gaps    3;

Qy    6 STPQTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLA 65
          | |    ::||  ||:   |||| |||||||||||||||||||||:| |||:|  :  ::
Db    2 SAPRTLYDKIWDDHVVNRDPDGTCLLYIDRHLVHEVTSPQAFEGLRIAGRPVHSPTRTLA 61

Qy   66 TTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLENVKEFGVTYFGLSDKRQGIVHVIGP 125
          ::|||||| :    :  ||||: |||||||| | |||| |||:: :::||||||||:|||
Db   62 VVDHNVPTTA-----DRLEGIKNESRIQVEALAQNAKEFGVEYYSERDKRQGIVHIVGP 116

Qy  126 EQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGE 185
        ||||||||:|:||||||||||||||||| |||||||||||||| ||   :||| :|||:
Db  117 EQGFTLPGMTIVCGDSHTSTHGAFGALAHGIGTSEVEHVLATQTLIQKKAKNMLVRVDGK 176

Qy  186 LAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMV 245
        | |||::||:||:|||:|||||||| :||  | :|||||||:||:|||||||||||||:|
Db  177 LPESVTAKDILAIIGEIGTAGGTGVIEVPAGEAIRSLSMEGRMTICNMSIEGGARAGLI 236

Qy  246 APDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWG 305
        |||| |||| ||||| ||   ||  ||::||| | ||:|| |||  : ||  ::|: :||
Db  237 APDETTFEYIKGRPRAPKGETLE--QAIAYWKTLKSDEGAHYDKVVILDDEGAHYDKVVILDAANLPPIVSWG 294

Qy  306 TSPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSR 365
        :|||| |::|:||::|:: |:|::|:|  |:|:||||| || | || : |||||||||:|
Db  295 SSPEDVTSVEGIVPNPDDIEEENKRTSKWKRTSKWRALDYMGLKPGTRITDIAIDRVFIGSCTNGR 354

Qy  366 IEDLRAAAAVKGRKKAPNVKSAMVVPGSGLVKTQABEEGLDKIFEEAGFEWREAGCSMC 425
        ||||||| :: ||:|  .   :|:|||||||| || |:||.||| :||| |||.|||||
Db  355 IEDLRAAAKIVDGRKVASTV-SAMIVPGSGLVKEQAEKEGLDKIFLDAGFEWREPGCSMC 413

Qy  426 LGMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRK 479
        | :| | | |:|||||||||||||||| : |||::||.|||||.| || ||.:|
Db  414 LAMNDDRLKPGERCASTSNRNFEGRQGYKSRTHLVSPAMAAAAAIAGHFVVSPAMAAAAAIAGHFVVRE 467

RESULT 12
LEU2_RHILO
ID  LEU2_RHILO   STANDARD;      PRT;    469 AA.
AC  Q98BF1;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE  (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
```

GN   LEUC OR MLL4272.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC   and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmalate = 3-isopropylmalate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC   H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC   isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC   SUBFAMILY.
CC   ---
CC   ---
DR   EMBL; AP003003; BAB50968.1; -.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   METAL   350   350   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL   410   410   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL   413   413   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   469 AA; 50871 MW; 64152D3D4F06888 CRC64;

Query Match   38.7%;
Best Local Similarity   64.1%;
Matches 307; Conservative   53; Mismatches 108; Indels   11; Gaps   4;

Score 1567.5; DB 1; Length 469;
Pred. No. 1.4e-98;

Qy   6 STPQTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRPDCTLA   65
           |::|||||| ||||:|||||| ||||||||||||||||||:||| ||||||| |||
Db   2 SAPRTLYDKFPDDHVDRQDDGTCLLYIDRHLVHEVTSPQAFEGLRLSGRKVRHPEKTLA   61

Qy   66 TTDHNVPFTTSRKALKDIASFIKEDDSRTQCCVTLEENVKEFGVTYFGLSDKRQGIVHVIGP 125
           |||||| | ||| || | ||::||:| | | || :|||:| |:||||||||:||
Db   62 VVDHNVSTSPERKFG-----IKNEESRIQVEALAKNAXDFGVEYYSENDIRQGIVHIIGP   116

Qy   126 EQGFTLPGTTVVCGDSHSTHCAFGALAFGIGTSEVEHVLATQCLIITKRSKNMRIQVDGE 185
           |||||||| |:||||||||||| ||| ||||||||||||||| || ||: ||| |||:
Db   117 EQGFTLPGMTIVCGDSHSTHGAPGALAHGIGTSEVEHVLATQTLIQRAKQNMLVRVDGQ   176

Qy   186 LAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMV 245
           | .||::||:: ||| |||||||| ||||.| ||||||| ||:||||||||||||:
Db   177 LPEGVTAXDIIAIIGIEIGTAGGTGYVIEYAGEAIRSLSMEGRMTICNMSIEGGARAGLI   236

Qy   246 APDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWG 305
           |.||:||.|:| :|.||| | .|| | |||.||||:|| :| ||:|| |:.| | ||
Db   237 AADETTFAYVKDKPRAPK--GAAWDAALAYWKTLQSDEGAHFDKVIVLDAAKLPPIVSWG 294

Db   306 TSPEDVVPITGVVPDPETFATEAKKADAGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSR 365
           :|||| : |||| || :|: |: . ||| |||| ||.::|| :||:||||||| |
Qy   306 SSPEDVSVSQGVVPNPEEITDENKRTSKIRALDYMGLTPGTIKITDIALDRVFIGSCTNGR 354

Db   366 IEDLRAAAAVVGRKKAPNVKSAMVPGSGLVKTQAEEBGLDKIFEEAGFEWREAGCSMC   425
           |||||||| |.|||||||||||||||||||:||||:||||||| |||| |||.|||| |
Qy   366 IEDLRAAAAVKGRKKAPNVKSAMVPGSGLVXTQAEBEGLDKIFEEAGFEWREAGCSMC   425

Db   426 LGMNPDIIAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKLTDYK 484
           : :| :: | ||:|||||||||||||| ||||| ||.:|||| |.|:| | |:| |
Qy   426 IEDLRAAAKVIEGKTVNPRV-NAMIVPGSGLVKEQAEREGLDKIFLAAGFDWREPGCSMC 413

Db   414 LAMNDDRLKPHERCASTSNRNFEGRQGFKGRTHLVSPAMAAAAIAGHFVDIR---DWK   469

RESULT 13

ID   LEU2_CAUCR   STANDARD;   PRT;   479 AA.
LEU2_CAUCR
AC   Q9AEN0;
RN   [1]
RP   SEQUENCE FROM N.A.
OX   NCBI_TaxID=155892;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR CC0196.
OS   Caulobacter crescentus.
OC   Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC   Caulobacter.
STRAIN=ATCC 19089 / CB15;
RC
RX   MEDLINE=21173698; PubMed=11259647;
RA   Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA   Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA   Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA   DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA   Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA   Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA   Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT   "Complete genome sequence of Caulobacter crescentus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC   and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmalate = 3-isopropylmalate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC   H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC   isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC   SUBFAMILY.
CC   ---
CC   ---
DR   EMBL; AE005694; AAK22183.1; -.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   METAL   350   350   IRON-SULFUR (4FE-4S) (BY SIMILARITY).

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FT   METAL         415  415   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL         418  418   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   479 AA;  50693 MW;  8E19EB931A251BFA CRC64;

Query Match
Best Local Similarity  38.5%;   Score 1562;  DB 1;  Length 479;
                       Conservative  64.4%;  Pred. No. 3.5e-98;
Matches  307;  Conservative  53;  Mismatches 105;  Indels  12;  Gaps  5;

Qy    9  QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD  68
         :||::| ||||: ||:|||||||||||||||:||||||||||||||||||||
Db    4  KTLYDKIWDAHVVSE-AGGEAILYIDLHLIHEVTTPQAFAGLRAAGRKVRRPDRTLAVAD  62

Qy   69  HNVPFTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG  128
         |:| |||:|| ::| |||||||:: :|||||: |::| ||||: :||| ||||||
Db   63  HNIPTEGQALGVDA---VADEEARLQLKTLARNVADNGIEFFPMGDIRNGIVHVGPEQG  119

Qy  129  FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP  188
         |||||||||||||||||||||||||||||||||||||:|| ::||:  ||::|
Db  120  RTQPGMTIVCGDSHTSTHGAFGALAHGIGTSEVEHVLATQTILRQKKAKNMLVRVDGQLPP  179

Qy  189  GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD  248
         ||: |:| : || |||||::| |||:||||:::|: || :||: |||:: ||||||||
Db  180  GVTGKDVALAVIGEIGTAGGTGYVIEFAGEAIAGLSMEGRMTLCNLTIEGGAKAGLVAPD  239

Qy  249  EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP  308
         ::||:|:|| |   :  :  | |||||||||||||||||||||||| |:|| |||:|||
Db  240  DKTFAYIQGKPAAPK--GAAWDMALSHWKIFFTDEDAVFDRTVVIDGSALVPMVTWGTSP  297

Qy  309  EDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIED  368
         ||::|: || ||:: |:|: |||| :|||:|||||| |:||||||||||||||||||||
Db  298  EDVIPVTGNVPDPESFATPDKRAAAHRALDYMGLKAGQPISEARIDRVFIGSCTNSRIED  357

Qy  369  LRAAAAVVK-----GRKKAPNVKSAMVVPGSGLVKTQABEEGLDKIFEEAGFEWREAGCS  423
         ||||||:     ||: :|||:|||||||||||:|:||||||||||::||:: || ||||
Db  358  MRAAAAVVQBAFLHGRLVAPHVK-AMVVPGSGLVKEQABEEGLDAIFKAAGFDWREPGCS  416

Qy  424  MCLGMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL  480
         ||| ||||:||||||||||||||||||||||||||||||:||||||:||||:||||
Db  417  MCLAMNPDKLAPQERCASTSNRNFEGRQGRAGRTHLVSPAMAAAAIAGHLVDVRTL  473


RESULT 14
LEU2_NEIMB
ID   LEU2_NEIMB   STANDARD;  PRT;  469 AA.
AC   Q9JZI5;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR NMB1036.
OS   Neisseria meningitidis (serogroup B).
OC   Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX   NCBI_TaxID=491;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MC58 / Serogroup B;
RX   MEDLINE=20175755; PubMed=10710307;
RA   Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA   Eisen J.A., Ketchum K.A., DeBoy R.T., Peterson J.D., Dodson R.J.,
RA   Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA   Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA   Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
RA   Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA   Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA   Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT   "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT   MC58.";
RL   Science 287:1809-1815(2000).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
```

```
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC       SUBFAMILY.
CC   --------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------
DR   EMBL; AE002454; AAF41435.1; -.
DR   TIGR; NMB1036; -.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   METAL        349   349   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL        410   410   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL        413   413   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   469 AA;  50843 MW;  D538C334B590E4E0 CRC64;

Query Match
Best Local Similarity  38.2%;   Score 1548.5;  DB 1;  Length 469;
                       Conservative  63.6%;  Pred. No. 2.7e-97;
Matches  302;  Conservative  62;  Mismatches 102;  Indels  9;  Gaps  3;

Qy    7  TPQTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLAT  66
         ||:||||: || |:::|:|||||||||:||:||||||||:|||::||:
Db    2  TAQTLYDKLWNSHVVREEEDGTVLLYIDRHLVHEVTSPQAFEGLKMAGRKLWRIDSVVST  61

Qy   67  TDHNVPFTSRKALKDIASFIKEDDSRTQCVTLEENVKEFG-VTYFGLSDKRQGIVHVIGP  125
         | :|:  |::::||| | :|      | ||||::||||| |:| ||| |||| ||||:
Db   62  ADHNTPT------GDWDKGIQDPISKLQVDTLDKNIKEFGALAYFPFMDKGQGIVHVMGP  115

Qy  126  EQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGE  185
         ||| ||||||||||||||||||||||||||||||||||||::  |:|::||::|::|:
Db  116  EQGATLPGMTVVCGDSHTSTHGAFGALAHGIGTSEVEHTMATQCITAKKKSKSMLISVDGK  175

Qy  186  LAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMV  245
         |||:||||||:| : | |||:|||||||||||::::|::||:| :|: ||||||:|||||
Db  176  LKAGVTAKDVALYIIGQIGTAGGTGYAIEFGGEAIRSLSMBSRMTLCNMAIEAGARSGMV  235

Qy  246  APDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWG  305
         |::| ||:|:||| | :   :| | ||||::|::: |::|:|:::|| |:| ||:||::
Db  236  AVDQTTIDYVKDKPFAPEGEA--WDKAVEYWRTLVSDEGAVFDKEYRFNAEDIEPQVTWG  293

Qy  306  TSPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSR  365
         |||::|:  :|| ||:: |: || |||| :||::|||| |:|||:|::||:||||||||
Db  294  TSPEMVLDISSKVPNPAETDPVKRSGMERALEYMGLEAGTPLNEIPVDIVFIGSCTNSR  353

Qy  366  IEDLRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMC  425
         ||||:|||| |:|::::|: ::| :| || ||:||||:|:||||||:||:|||||||||||
Db  354  IEDLREAAAIAKDRKKAANVQRVLIVPGSGLVKEQAEKEGLDKIFIEAGFEWREPGCSMC  413

Qy  426  LGMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL  480
         |||| :|||||||||||||||||||||| ||||:|||:|||||| :||:|||| :
Db  414  LAMNADRLTPGQRCASTSNRNFEGRQNGGRTHLVSPAMAAAAAVTGRFTDIRMK  468


RESULT 15
LEU2_NEIMA
ID   LEU2_NEIMA   STANDARD;  PRT;  469 AA.
AC   Q9JU82;
DT   15-JUN-2002 (Rel. 41, Created)
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DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR NMA1450.
OS   Neisseria meningitidis (serogroup A).
OC   Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX   NCBI_TaxID=65699;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX   MEDLINE=20222556; PubMed=10761919;
RA   Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA   Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA   Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA   Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA   Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA   Whitehead S., Spratt B.G., Barrell B.G.;
RT   "Complete DNA sequence of a serogroup A strain of Neisseria
RT   meningitidis Z2491.";
RL   Nature 404:502-506(2000).
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DR   EMBL; AL162756; CAB84686.1; -.
DR   InterPro; IPR001030; Aconitase.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   METAL       349    349       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       410    410       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       413    413       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   469 AA;  50783 MW;  89AE349827DA25DB CRC64;

Query Match             38.1%;  Score 1545.5;  DB 1;  Length 469;
Best Local Similarity   63.4%;
Matches  301;  Conservative   62;  Mismatches  103;  Indels    9;  Gaps    3;
                               Pred. No. 4.4e-97;

Qy      7 TPGTLYDKVLQAHVVDEKLDGTIVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLLAT 66
            |||| |||  |||  |||||.||||||||||||||||||||   |||| |    :||
Db      2 TAQTLYDKLWNSHVVREEBDGTVLLYIDRHLVHEVTSPQAFEGLKMAGRKLWRIDSVVST 61

Qy     67 TDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFG-VTYFGLSDKRQGIVHVIGP 125
          :|||  ||      ||    |  |||        ::|||||  |:|| :|||||||| |||
Db     62 ADHNTPT-----GDWDKGIQDPISKLQVDTLDKNIKEFGALAYFPFMDKGQGIVHVMGP 115

Qy    126 EQGFTLPGTTVVCGDSHSTHGAFGALAFGIGTSEVEHVLATQCLITRKSKNMRIQVDGE 185
          |||.|||| ||||||||||||||||||| |||||||||.:||||.| ||| | |:.|||
Db    116 EQGATLPGMTVVCGDSHSTHGAFGALAAHGIGTSEVEHTMATQCITTAKKSKSMLIAVDGK 175

Qy    186 LAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMV 245
          | .||::||| |:|||  ||.|||||.|||.|. |||||||.|| : |||:|.|||:|||
Db    176 LKAGVTAKDVALYIIGQITAGGTGYAIEFGGEAIRSLSMEGRMTLCNMAIEAGARSGMV 235

Qy    246 APDEITEYLKGRPLAPKYDSPEWHKATQYWKNLQSDFGAKYDIDVFIDAKDIVPTLTWG 305
           .|: | ::|  | ||  :  ::|||..||::|  |.||..|:| :::.|:| | .| ||
Db    236 AVDQTTIDVKDKPFAPEGBA--WDKAVEYWRTLVSDEGAVFDKEYRFNAEDIEPQVTWG 293

Qy    306 TSPEDVVPITGWVDPEETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSR 365
          |||| |: |:. | |.|   :.  ||  :| | ||||:|||| |:|||| |||||||||||
Db    294 TSPEMVLDISSKVPNPAEETDPVKRSGMERALEYMGLEAGTPLNEIPVDIVFIGSCTNSR 353

Qy    366 IEDLRAAAVVKGRKKAPNVKSANVPGSGLVKTQAEEBGLDKIFEEAGFEWREAGCSMC 425
          :|||  |||.|.|||| ||   :: ||||||.||||.|||||| ||||||||.|||||
Db    354 VEDLREAAIAKDRKKAANVQRVLIVPGSGLVKEQAEKBGLDKIFIEAGFEWREPGCSMC 413

Qy    426 LGMNPDLLAPQBRCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLLADVRKL 480
          | ||  :  |.|||||||||||||| | ||||||:||.|||||.:.|:    :| :|
Db    414 LAMNADRLTPGQRCASTSNRNFEGRGNGGRTHLVSPAMAAAAVTGRFTDIRMM 468
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RESULT 16
ID   LEU2_XANCP     STANDARD;      PRT;   479 AA.
AC   P58949;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR XCC3331.
OS   Xanthomonas campestris (pv. campestris).
OC   Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC   Xanthomonas.
OX   NCBI_TaxID=340;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33913 / NCPPB 528;
RX   MEDLINE=22022145; PubMed=12024217;
RA   da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA   Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA   Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA   Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA   Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA   Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA   Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA   Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA   Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA   Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA   Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA   Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA   Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA   Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA   Setubal J.C., Kitajima J.P.;
RT   "Comparison of the genomes of two Xanthomonas pathogens with differing
RT   host specificities.";
RL   Nature 417:459-463(2002).
```

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RA      Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA      Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA      Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA      Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA      Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA      Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA      Setubal J.C., Kitajima J.P.;
RT      "Comparison of the genomes of two Xanthomonas pathogens with differing
RT      host specificities";
RL      Nature 417:459-463(2002).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC       SUBFAMILY.
CC
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CC       or send an email to license@isb-sib.ch).
CC
DR      EMBL; AE011993; AAM38301.1; -.
DR      PROSITE; PS00450; ACONITASE_1; 1.
DR      PROSITE; PS01244; ACONITASE_2; 1.
KW      Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT      METAL        353        353       IRON-SULFUR (4FE-4S)   (BY SIMILARITY).
FT      METAL        414        414       IRON-SULFUR (4FE-4S)   (BY SIMILARITY).
FT      METAL        417        417       IRON-SULFUR (4FE-4S)   (BY SIMILARITY).
SQ      SEQUENCE   479 AA;  51506 MW;  70111DB3123FB0A6 CRC64;

Query Match             37.3%;  Score 1514.5;  DB 1;  Length 479;
Best Local Similarity   63.5%;  Pred. No. 5.6e-95;
Matches  301;  Conservative   51;  Mismatches  119;  Indels    3;  Gaps    2;

Qy      7   TPQTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLAT  66
                :||::|| :||:| |::::|  ||||||:|::||||||||||||::|:|:|:|||
Db      2   TARTLYDKLWELHEVTRRDDGSSLIYIDRHILHEVTSPQAFEGLRLLAGRKPWRIDANIAT  61

Qy      67  TDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPE  126
                |||||||||  || |: ::|:    ||: |||||||:|||||||||:::|||||||||
Db      62  PDHNVPTTRAERQGGLES-ISDEVSRLQVTLDENCDDFGILEFKMNDARQGIVHVVGPE  120

Qy      127 QGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGEL  186
                |||:|||:||||||||||||||||| |:|||||||||||||:||:||:|:|:|||: :
Db      121 QGATLPGMTVVCGDSHTSTHGAFGALAHGIGTSEVEHVLATQCLIAKKMKNMQVRVEGTL  180

Qy      187 APGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVA  246
                ||||: |::||||||:||:|||:  :|  ||||:|:|:||||:||:|||:|||:| |||
Db      181 PFGVTAKDIVLAVIGKIGTAGGNGHALEFAGSAIRTLSMEGRMTICNMAIEAGARVGMVA  240

Qy      247 PDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVPIDAKDIVPTLTWGT  306
                ||:||||||||||| |:| :::|||||:|||::|:| ||||||||:|: |||:|| ||:
Db      241 VDEKTIAYVRGRPFAPK--GAHWDAAVALWRTLVSDADASFDTVVELRAEDIKPQVSWGT  298

Qy      307 SPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRI  366
                ||: |::|:||||| |  :|: || |:::||::||||||:|   |:|::||||||||||
Db      299 SPEMVLAIDQHVPDPAIEQDPTKRDSIERALKYMGLKANQPITAIRLDRVFIGSCTNSRI  358

Qy      367 EDLRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCL  426
                |||| ||||||:||| |||:|:|||||||||||:||| ::||||| |||||| | ||||
Db      359 EDLRAAAAVAKGRKVASTIKQALVVPGSGLVKAQAEAEGLDKVFLDAGFEWREPGCSMCL  418

Qy      427 GMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL  480
                 ||||  | :|||||||||||||||||||||:|:||:|| || :||:|||:|:|
Db      419 AMNPDKLGSGEHCASTSNRNFEGRQGAGGRTHLVSPAMAAAAVSGHFVDVREL  472
```

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CC
DR      EMBL; AE012450; AAM42601.1; -.
DR      PROSITE; PS00450; ACONITASE_1; 1.
DR      PROSITE; PS01244; ACONITASE_2; 1.
KW      Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT      METAL        353        353       IRON-SULFUR (4FE-4S)   (BY SIMILARITY).
FT      METAL        414        414       IRON-SULFUR (4FE-4S)   (BY SIMILARITY).
FT      METAL        417        417       IRON-SULFUR (4FE-4S)   (BY SIMILARITY).
SQ      SEQUENCE   479 AA;  51466 MW;  8E46023FEB703958 CRC64;

Query Match             37.5%;  Score 1522.5;  DB 1;  Length 479;
Best Local Similarity   63.7%;  Pred. No. 1.6e-95;
Matches  302;  Conservative   53;  Mismatches  116;  Indels    3;  Gaps    2;

Qy      7   TPQTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLAT  66
                :||::|| :||:| |::::|  ||||||:|::||||||||||||::|:|:|:|||
Db      2   TAKTLYDKLWEMHEVTRRDDGSSLIYIDRHILHEVTSPQAFEGLRLLAGRKPWRIDANIAT  61

Qy      67  TDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPE  126
                |||||||||  || |: ::|:    ||: |||||||:|||||||||:::|||||||||
Db      62  PDHNVPTTRAERQGGLES-ISDEVSRLQVTLDENCDDFGILEFKMNDTRQGIVHVVGPE  120

Qy      127 QGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGEL  186
                |||:|||:||||||||||||||||| |:|||||||||||||:||:|| |:|:|||: :
Db      121 QGATLPGMTVVCGDSHTSTHGAFGALAHGIGTSEVEHVLATQCLIAKKMKNLQVRVEGTL  180

Qy      187 APGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVA  246
                ||||: |::||||||:||:|||:  :|  ||||:|:|:||||:||:|||:|||:| |||
Db      181 PFGVTAKDIVLAVIGKIGTAGGNGHALEFAGSAIRALSMEGRMTICNMSIEAGARVGMVA  240

Qy      247 PDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVPIDAKDIVPTLTWGT  306
                ||:||||||||||| |:| :::|||||:|||::|:| ||||||||:|: |||:|| ||:
Db      241 VDEKTIAYVRGRPFAPK--GADWDAAVALWRTLVSDADASFDTVVELRAEDIKPQVSWGT  298

Qy      307 SPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRI  366
                ||: |::|:||||| |  :|: || |:::||::||||||:|   |:|::||||||||||
Db      299 SPEMVAIDQQVPDPAAEQDPTKRDSIQRALKYMGLRANQPITEIHLDRVFIGSCTNSRI  358

Qy      367 EDLRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCL  426
                |||| ||||||:||| |||:|:|||||||||||:||| ::||||| |||||| | ||||
Db      359 EDLRAAAAVAKGRKVASTIKQALVVPGSGLVKAQAEAEGLDKIFLDAGFEWREPGGCSMCL  418

Qy      427 GMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL  480
                 ||||  | :|||||||||||||||||||||:|:||:|| || :||:|||:|:|
Db      419 AMNPDKLGSGEHCASTSNRNFEGRQGAGGRTHLVSPAMAAAAVSGHFVDVREL  472
```

```
RESULT 17
LEU2_XANAC
ID   LEU2_XANAC     STANDARD;        PRT;    479 AA.
AC   P58948;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR XAC3458.
OS   Xanthomonas axonopodis (pv. citri).
OC   Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC   Xanthomonas.
OX   NCBI_TaxID=92829;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=306 / ATCC 13902 / XV 101;
RX   MEDLINE=22022145; PubMed=12024217;
RA   da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA   Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA   Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA   Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA   Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA   Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA   Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA   Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
```

RESULT 18

```
ID    LEU2_PSEAE     STANDARD;      PRT;   474 AA.
AC    Q9HZA3;
DT    15-JUN-2002 (Rel. 41, Created)
DT    15-JUN-2002 (Rel. 41, Last sequence update)
DT    15-JUN-2002 (Rel. 41, Last annotation update)
DE    3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE    (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN    LEUC OR PA3121.
OS    Pseudomonas aeruginosa.
OC    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC    Pseudomonas.
OX    NCBI_TaxID=287;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=ATCC 15692 / PAO1;
RX    MEDLINE=20437337; PubMed=10984043;
RA    Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA    Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA    Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA    Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA    Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA    Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT    "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT    opportunistic pathogen.";
RL    Nature 406:959-964(2000).
CC    -!- FUNCTION: Catalyzes the isomeriation between 2-isopropylmalate
CC        and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC    -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC        H(2)O.
CC    -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC        isopropylmalate.
CC    -!- PATHWAY: Leucine biosynthesis; second step.
CC    -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC    -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC        SUBFAMILY.
CC    --------------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use by non-profit institutions as long as its content is in no way
CC    modified and this statement is not removed. Usage by and for commercial
CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; AE004736; AAG06509.1; -.
DR    InterPro; IPR001030; Aconitase_N.
DR    InterPro; IPR004430; LeuC.
DR    Pfam; PF00330; aconitase; 1.
DR    PRINTS; PR00415; ACONITASE.
DR    ProDom; PD000511; Aconitase_N; 1.
DR    TIGRFAMs; TIGR00170; leuC; 1.
DR    PROSITE; PS00450; ACONITASE_1; 1.
DR    PROSITE; PS01244; ACONITASE_2; 1.
KW    Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT    METAL       353    353       Iron-sulfur (4FE-4S)  (BY SIMILARITY).
FT    METAL       414    414       Iron-sulfur (4FE-4S)  (BY SIMILARITY).
FT    METAL       417    417       Iron-sulfur (4FE-4S)  (BY SIMILARITY).
SQ    SEQUENCE   474 AA;  51042 MW;  7B4A0F65002228EC CRC64;
```

```
Query Match             37.2%;
Best Local Similarity   62.5%;
Matches  295;      Conservative  61;   Mismatches 113;   Indels   3;   Gaps   2;
```

```
Qy      9 QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD 68
            ||||| :| |:| :| |||||:|| |:||||| ||||| |||  |||||||:| |||||
Db      9 KTLYDKLWDMHLVKQRDDGSALIYIDRHILHEVTSPQAFEGLRLAGRKPWRIDANIATPD 63

Qy     69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKFEGVTYFGLSDKRQGIVHVIGPEQG 128
            ||||||:| ||| ||:| :| :|| |  |:||  ||| |  | :  ||: :  || ||
Db      4 HNVPTTRTERKGGIAA-IADEVSRLQVQTLDENCDDFGITEFKMNDVRQGIVHVVGPEQG 63
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RESULT 19

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ID    LEU2_XYLFA     STANDARD;      PRT;   474 AA.
AC    Q9PAX0;
DT    15-JUN-2002 (Rel. 41, Created)
DT    15-JUN-2002 (Rel. 41, Last sequence update)
DT    15-JUN-2002 (Rel. 41, Last annotation update)
DE    3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE    (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN    LEUC OR XF2375.
OS    Xylella fastidiosa.
OC    Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC    Xylella.
OX    NCBI_TaxID=2371;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=9a5c;
RX    MEDLINE=20365717; PubMed=10910347;
RA    Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA    Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA    Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA    Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA    Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA    Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA    Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA    Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA    Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA    Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA    Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA    Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA    Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA    Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA    Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA    Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA    Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA    de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA    Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA    Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA    de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA    da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA    da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA    de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA    Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA    Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT    "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL    Nature 406:151-159(2000).
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Qy     64 HNVPTTRTERKGGIAA-IADEVSRLQVQTLDENCDDFGITEFKMNDVRQGIVHVVGPEQG 122
            || ||  |||: || ||| |:|||| :||||  :||| | |  |:|||||||||||||
Db    129 FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLLTKRSKNMRIQVDGELAP 188

Qy    123 ATLPGMTVVCGDSHTSTHGAFGALAHGIGTSEVEHVLATQCLVAKKMKNMLVKYEGRLPA 182
            ||||||||||||||||||||||||| |||||||||||||||| ||:||||||| |||||
Db    123 ATLPGMTVVCGDSHTSTHGAFGALAHGIGTSEVEHVLATQCLVAKKMKNMLVKYEGRLPA 182

Qy    189 GVSSKDVVLHAIGIIGTTAGGTGAVIECGSVIRSLSMEARMSICNMSIEGGARAGMVAPD 248
            ||::|||||:||| |||| || || |||||| |||| || | ||||||||||||||| |
Db    189 GVTAKDIVLAVIGRIGTTAGGNGHAIEFAGSAIRDLSIEGRMTICNMSIEAGARGLVAVD 242

Qy    249 EITFEYLKGRPLAPKYDSPEWHKATQVWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP 308
            :|:|| :||||:|:|  |  :|:||   ||||  |  : ||| :||:|  | |  |||||
Db    243 QKTIDVVKGRPAP--SABQWIDGAVACWQGLVSDADARPDTVVELDAAQIKPQVSWGTSP 300

Qy    309 EDVVPIGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIIPVDKVFIGSCTNSRIED 368
            |:|| |||:|||:  ||| |:|      | ||:  || |:: |:|:|  |||||||||||
Db    301 EMVLAVDQNVPDPARESDPIKRGSIERALKYMGLRPNQAITDIQLDRVPIGSCTNSRIED 360

Qy    369 LRAAAVKGRKKAPNVKSAMVVPGSGLVKVTQAEEEGLDKIFEEAGFEWREAGCSMCLGM 428
            ||||  | || || |:| || |||||||:    ||||| |||||||||||| |||| ||
Db    361 LRAAAEVARGRKVAATIKQALVVPGSGLVKEQAPEKEGLDRIFIEAGFEWREPGCSMCLAM 420

Qy    429 NPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL 480
            |||:| ||:|||||||||||||||||||||:|:||||||| |:||:|||  :
Db    421 NPDRLESGEHCASTSNRNFEGRQGAGGRTHLVSPAMAAAAAVANGRFIDVREL 472
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ID   LEU2_RALSO               STANDARD;      PRT;   469 AA.
AC   Q8XXX3;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR RSC1990 OR RS03558.
OS   Ralstonia solanacearum (Pseudomonas solanacearum).
OC   Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC   Ralstonia.
OX   NCBI_TaxID=305;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GMI1000;
RX   MEDLINE=21681879; PubMed=11823852;
RA   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA   Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA   Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA   Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA   Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA   Weissenbach J., Boucher C.A.;
RT   "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL   Nature 415:497-502(2002).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC       SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long  as its content  is in  no  way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AL646067; CAD15692.1; -.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   METAL       347    347       Iron-sulfur (4FE-4S) (BY SIMILARITY).
FT   METAL       410    410       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       413    413       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   469 AA;  50796 MW;  B451E96E44788AAE CRC64;
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Query Match             36.8%;   Score 1493;  DB 1;  Length 469;
Best Local Similarity   63.5%;   Pred. No. 1.5e-93;
Matches  301;  Conservative  53;  Mismatches 110;  Indels  10;  Gaps  3;

Qy      9 QTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD 68
            ||||: | |  ||::::  .|| :| ::||||||||||||:||||  |   |::|:|||
Db      3 KTLYDKLWDDHVHTEEDGTTVLYIDRQLLHEVTSPQAFEGLKLANRPVWRISANLAVSD 62

Qy     69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG 128
           |||||||:.|   | ||:||:|| | : || :::: :||| ::||:   ||:|||||||||
Db     63 HNVPTTDR------SHGIADPVSKLQVDTLDANCDSFGITQFKMTDKRQGIVHVIGPEQG 116

Qy    129 FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
           ||||||||||||||||||||||||||||||||||||||||||:|::||||: ||::| |
Db    117 ATLPGMTVVCGDSHTSTHGAFGALAHGIGTSEVEHVLATQTLLAKKSKNMLVKVEGTLPR 176
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RESULT 20
LEU2_RALSO
```

```
Qy   189 GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD 248
             |: ||:|.||:..|||||||:|:|||..|:|.||||.:|.|:||:|.|||||||...|
Db   177 GCTAKDIVLAIIGKIGTAGGTGYAMEFGGSAIRALSMEGRMTVCNMAIEAGARAGMVGVD 236

Qy   249 EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP 308
             .||.||:|||.||:  .|.|.:||.:||:.|.|.:||:|.|.::..::||| :||||||
Db   237 DITLEYIKGRPFAPQ--GVEWEQAVAYWRSLHSDEGARFDHVVELRAEEIRPQVSWGTSP 294

Qy   309 EDVVPITGVVPDPETFATEAKKADGRRMLQYMGLIKAGTPMEDIPVDKVFIGSCTNSRIED 368
             |.||.|..|||||:.. :.|.:.|.||.:. |.|:|...:.|.|.|:||||||||||||:|
Db   295 EMVVSIEDRVPDPDKEKDPVKRNAMERALEYMALQPNVAIGDIRIDKVFIGSCTNSRIED 354

Qy   369 LRAAAAVVK--GRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCL 426
             :|||||||:  |:|:|.||| :||||||||||.||| ||||||||:.||||||.|||||
Db   355 MRAAAAVVQKLGKRIASNVKLAMVVPGSGLVKEQAEREGLDKIFKAAGFEWREPGCSMCL 414

Qy   427 GMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLLADVRKL 480
             .||.|.|.|.||||||||||||||||||||||:.||.|||||.:.|.:|.|||||
Db   415 AMNADRLEPGERCASTSNRNFEGRQGAGGRTHLVSPAMAAAAALEGHHVDVRKL 468
```

RESULT 21
LEU2_ECOLI

ID   LEU2_ECOLI   STANDARD;   PRT;   465 AA.
AC   P30127; P78042;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR B0072.
OS   Escherichia coli.
OC   Escherichia; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91088346; PubMed=2124684;
RA   Rosenthal E.R., Calvo J.M.;
RT   "Aphidicolin inhibits DNA polymerase II of Escherichia coli, an
RT   alpha-like DNA polymerase.";
RL   Nucleic Acids Res. 18:7185-7186(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92334977; PubMed=1630901;
RA   Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RA   Isono K., Mizobuchi K., Nakata A.;
RT   "Systematic sequencing of the Escherichia coli genome: analysis of
RT   the 0-2.4 min region.";
RL   Nucleic Acids Res. 20:3305-3308(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [4]
RP   SEQUENCE OF 1-203 FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=94164169; PubMed=8119295;
RA   Kirino H., Aoki M., Hayashi Y., Ohba M., Yamagishi A., Wakagi T.,
RA   Oshima T.;
RT   "Hydrophobic interaction at the subunit interface contributes to the
RT   thermostability of 3-isopropylmalate dehydrogenase from an extreme
RT   thermophile, Thermus thermophilus.";
RL   Eur. J. Biochem. 220:275-281(1994).
RN   [5]
RP   SEQUENCE OF 1-12;
RC   STRAIN=K12 / EMG2;
RX   MEDLINE=97443975; PubMed=9298646;
RA   Link A.J., Robison K., Church G.M.;
RT   "Comparing the predicted and observed properties of proteins encoded
RT   in the genome of Escherichia coli K-12.";
RL   Electrophoresis 18:1259-1313(1997).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC   and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC   H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC   isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD.
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC   SUBFAMILY.
CC   -!-

DR   EMBL; D17632; BAA21005.1; -.
DR   EMBL; D10483; BAB96641.1; -.
DR   EMBL; AE000117; AAC73183.1; -.
DR   EMBL; D17631; BAA21004.1; -.
DR   SWISS-2DPAGE; P30127; COLI.
DR   EcoGene; EG11576; leuC.
DR   Interpro; IPR001030; Aconitase.
DR   Interpro; IPR001030; Aconitase_N.
DR   Interpro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   INIT_MET   0   0
FT   METAL   346   346   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL   406   406   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL   409   409   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   CONFLICT   70   70   D -> G (IN REF. 1 AND 2).
FT   CONFLICT   73   73   A -> G (IN REF. 4).
FT   CONFLICT   270   270   MISSING (IN REF. 1).
FT   CONFLICT   451   453   MISSING (IN REF. 1).
SQ   SEQUENCE   465 AA; 49778 MW; 0D085F17E89816A CRC64;

Query Match   36.6%;
Best Local Similarity 62.3%;
Matches 294; Conservative   59; Mismatches 110; Indels   9; Gaps   4;

Score 1483.5; DB 1; Length 465;
Pred. No. 6.7e-93;

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Qy     9 QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD 68
           :|||:||:.|||| :.....|:|||||||||||||||||.||..|||.||.|..|.|:.|
Db     2 KTLYEKLFDAHVVYEAENETPLLYIDRHLVHEVTSPQAFDGLRAHGRPVRQPGRTFPATMD 61

Qy    69 HNVPTISRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQ 128
           |||.| :.|  ||||.:.    ||:|.  |:.|:|:.|:|:.|:.||.|:|||||:|||
Db    62 HNVSTQT---KDINAC--GEMARIQMQELIKNCKEFGVELYDLNHPYQGIVHVMGPEQ 115

Qy   129 FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLIITKRSKNMRIQVDGELAP 188
           :|||||:|||||||||:|||||||||||||||||||||.|.|:..|:..:|||:|.|:.|
Db   116 VTLPGMTIVVCGDSHTATHGAFGALAFGIGTSEVEHVLATQTLKQGRAKMKIEVQGKAAP 175

Qy   189 GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD 248
           |:::|||:|.||||.|::||||||:||||.:||.||||.|:::|||:||.||:||:|||||
Db   176 GITAKDIVLAIIGKTGSAGGTGHVVEFCGEAIRDLSMEGRMTLCNMAIEMGAKAGLVAPD 235

Qy   249 EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP 308
             .||.||:|||.||:  .|.|.:||.:||:.|.|.:||:|.|.::..::||| :|||
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Db   236  ETTFNYVKGRLHAPK--GKDFDDAVAYWKTLQTDEGATFDTVVTLQAEEISPQVTWGTNP 293
          |||:|       ::     .:: .   :||||     :||||||||||||
Qy   309  EDVVPITGVVPDPETFATEAKKADGRRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIED 368
          |||||||:||||||    ||| .::    ||||| |||||||||||||||||||
Db   294  GQVISVNDNIPDPASFADPVERASAEKALAYMGLKPGIPLTEVAIDKVFIGSCTNSRIED 353

Qy   369  LRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWRREAGCSMCLGM 428
          ||||| |  :|:||    |: |||||:|| ||||| |||||||| ||||| ||||| |||
Db   354  LRAAAEIVKGRKVAPGVQ-ALVPGSGPVKAQAEAEGLDKIFIEAGFEWRLPGCSMCLAM 412

Qy   429  NPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL 480
          ||| | ||||||||||||||||| |:|| |||||:|   :::|:
Db   413  NNDRLNPGERCASTSNRNFEGRQGRGGRTHLVSPAMAAAAAVTGHFADIRNI 464

RESULT 22
LE21_SALTY
ID   LE21_SALTY     STANDARD;     PRT;     465 AA.
AC   P15777;
DT   01-APR-1990 (Rel. 14, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit 1 (EC 4.2.1.33)
DE   (Isopropylmalate isomerase 1) (Alpha-IPM isomerase 1).
GN   LEUC1 OR LEUC OR STM0111.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RX   MEDLINE=9272436; PubMed=2190189;
RA   Rosenthal E.R., Calvo J.M.;
RT   "The nucleotide sequence of leuC from Salmonella typhimurium.";
RL   Nucleic Acids Res. 18:3072-3072(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC       SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X51476; CAA35840.1; -.
DR   EMBL; M31047; AAA27155.1; -.
DR   EMBL; AE008699; AAL19075.1; -.
DR   PIR; S10171; S10171.
DR   StyGene; SG10197; leuC1.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   INIT_MET       0      0
FT   METAL        346    346       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL        406    406       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL        409    409       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   CONFLICT      37     53       PQAFDGLRAHHRPVRQP -> RRRLTVCARTIAGTSA (IN
FT                                 REF. 1).
FT   CONFLICT     345    345       S -> P (IN REF. 1).
FT   CONFLICT     357    357       A -> P (IN REF. 1).
FT   CONFLICT     361    364       AKGR -> GQRA (IN REF. 1).
FT   CONFLICT     368    384       PGVQALVVPGSGPVKAQ -> GRAGAGAGFRSGESA (IN
FT                                 REF. 1).
FT   CONFLICT     410    412       LAM -> VAV (IN REF. 1).
SQ   SEQUENCE   465 AA;  49654 MW;  014ED81AF5A19BB7 CRC64;

Query Match                   36.4%;  Score 1477.5;  DB 1;  Length 465;
Best Local Similarity         61.7%;  Pred. No. 1.7e-92;
Matches 291;   Conservative   63;   Mismatches 109;   Indels   9;   Gaps   4;

Qy     9  QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD 68
          || | |:     ||: ::   :||||||||||||||||||:  |: :: |::|  :||:
Db     2  KTLYEKLFDAHVVFEAPNETPLLYIDRHLVHEVTSPQAFQDGLRAHHRPVRQPGKTFATMD 61

Qy    69  HNVPTTSRALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG 128
          |||:|        |.|  :     ||.:: ::|:||: :||||.  : |||:|||:|||
Db    62  HNVSTQT----KDINA--SGEMARIQMQELIKNCNEFGVELYDLNHPYQGIVHVMGPEQG 115

Qy   129  FTLEGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
          ||||||||||||||:|||||||||||||||||||||||:||||||:||||||||||||||
Db   116  VTLPGMTIVCGDSHTATHGAFGALAFGIGTSEVEHVLATQTLKQGRAKTMKIEVTGNAAP 175

Qy   189  GVSSKDVLHAIGIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD 248
          |:  :||||:|||||:|||:|||||||||||:||:|||:|||:|::|:||||:|||||
Db   176  GITAKDIVLAIIGKTGSAGGTGHVEFCGDAIRALSMEGRMTLCNMAIEMGAKAGLVAPD 235

Qy   249  EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP 308
          |||||||||||||||  ||||:||:|::   :|: ||| ||||||:||||||||||||||
Db   236  ETTFNYVKGRLHAPK--GRDFDEAVEYWKTLKTDDGATFDTVVALRAEEIAPQVTWGTNP 293

Qy   309  EDVVPITGVVPDPETFATEAKKADGRRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIED 368
          |||||||:||||||    ||| .::    ||||| |||||||||||||||||||
Db   294  GQVISVTDIIPDPASFSDPVERASAEKALAYMGLQGVPLTDVAIDKVFIGSCTNSRIED 353

Qy   369  LRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGM 428
          ||||| |  :|:||    |: |||||:|| ||||| |||||||| ||||| ||||| |||
Db   354  LRAAAEVAKGRKVAPGVQ-ALVPGSGPVKAQAEAEGLDKIFIEAGFEWRLPGCSMCLAM 412

Qy   429  NPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL 480
          ||| | ||||||||||||||||| |:|| |||||:|   :::|:
Db   413  NNDRLNPGERCASTSNRNFEGRQGRGGRTHLVSPAMAAAAAVTGHFADIRSI 464

RESULT 23
LEU2_SALTI
ID   LEU2_SALTI     STANDARD;     PRT;     465 AA.
AC   Q8ZQI2;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR STY0130.
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
```

RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC   and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC   H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC   isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC   SUBFAMILY.
CC   --

DR   EMBL; AL627265; CAD01268.1; -.
DR   InterPro; IPR001030; Aconitase_N.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   INIT_MET   0   0   BY SIMILARITY.
FT   METAL   346   346   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL   406   406   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL   409   409   IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   465 AA; 49684 MW; 4C23A8068CC492DB CRC64;

Query Match   36.4%;
Best Local Similarity   61.7%;
Matches 291; Conservative   63; Mismatches 109; Indels   9; Gaps   4;

Score 1477.5; DB 1; Length 465;
Pred. No.1.7e-92;

Qy   9 QTLYDKVLQAHVDEKLDGTVLLIYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD 68
                ||||:|||||||||||:||||||:||||||:||||||:||||||:||||||||:|||||
Db   2 KTLYEKLFDAHVFEAPNETPLLYIDRHLVHEVTSPQAFDGLRAHHRPVRQPGKTFATMD 61

Qy   69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG 128
                ||:|||:||||||||:   :||||:||||:|:|:|:||||:||||:|||:||:||||||||
Db   62 HNVSTQT---KDINA--SGEMARIQMOELIKNCNEFGVELIYDLNHPYQGIVHVMGPEQG 115

Qy   129 FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
                |:|:||||:|||||||||||||||||:|||||||||:||:||||||||||||||||||:|
Db   116 VTLPGMTIVCGDSHTATHGAFGALAFGIGTSEVEHVLATQTILKQGRAKMKIEVTGNAAP 175

Qy   189 GVSSKDVVLHAIGIIGTGAGGVAIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD 248
                |||||||:|:|||:||||||||||||||||||:|||:|||||||||::|||||||||||
Db   176 GITAKDIVLAIIGKTSSAGGTGHVVEFCGDAIRALSMEGRMTLCNMAIEMGAKAGLVAPD 235

Qy   249 EITFEYLKGRPLAPKYDSPEWHKATQVWKNLQSDPGAKYDIDVPIDAKDIVPLTWGTSP 308
                :|||:|:|||||||||:|||||||||:|||||:|||||||||:|||||||||||:||||
Db   236 ETTFNYVKGRLHAPK---GRDFDEAVEWKTLKDDGATFDTVVTLRAEIAPQVTWGTNP 293

Qy   309 EDVVPITGVPPDPETFATEAKADGRRMLQYGLKAGTPMEDIIPVDKVFIGSCTNSRIED 368
                :||::||:|:||||:|||:||||:|:|:|:|||:||:|||::||:||||||||||||||
Db   294 GQVISVTDIIPDPASFSDPVERASAEKALLAYMGLQPGVPLTDVAIDKVFIGSCTNSRIED 353

Qy   369 LRAAAAVVKGRKKAPNYKSAMVPVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGM 428
                :||||||||||||||||||||::|||||||||:||||||||||||||||||||||||||||
Db   354 LRAAAEVAKGRKVAPGVQ-ALVVPGSGPVKAQAEAEGLDKIFIEAGFEWRLPGCSMCLAM 412

Qy   429 NPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL 480
                ||:||||||||||||||||||||:|:|:|||||||||||||||:|||:|::|
Db   413 NNDRLNPGERCASTSNRNFEGRQGRGGRTHLVSPAMAAAAVTGIHFADIRSI 464

RESULT 24
ID   LEU2_HAEIN   STANDARD;   PRT;   468 AA.
AC   P44968;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR HI0988.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Rd / KW20 / ATCC 51907;
RX   MEDLINE=95350630; PubMed=7542800;
RA   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA   Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G., Fitzhugh W., Fields C., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA   Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA   Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA   Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA   Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA   Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT   Rd.";
RL   Science 269:496-512(1995).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC   and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC   H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC   isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC   SUBFAMILY.
CC   --

DR   EMBL; U32779; AAC22649.1; -.
DR   TIGR; HI0988; -.
DR   InterPro; IPR001030; Aconitase_N.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   INIT_MET   0   0   BY SIMILARITY.
FT   METAL   346   346   IRON-SULFUR (4FE-4S) (BY SIMILARITY).

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FT   METAL         407    407       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL         410    410       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE    468 AA;  50743 MW;  0F6AFAF97AAAE9F6 CRC64;

Query Match            36.3%;  Score 1471;  DB 1;  Length 468;
Best Local Similarity  59.4%;  Pred. No. 4.7e-92;
Matches   281;  Conservative  72;  Mismatches 112;  Indels   8;  Gaps  2;

Qy     9  QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD 68
             :|||| :|: : |    :: |||| |||||||||||||||||: ||: |:|
Db     2  KTLYEKLFDSHIVYEAEGETPLLYINRHLIHEVTSPQAFDGLRVANRQVRQVNKTFGTMD 61

Qy    69  HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG 128
             : |          ||||||||||||||||||||||||||: |:|||||||||||||
Db    62  -------LEGQAKIQVLELDKNTKATGIKLKFDITTKEQGIVHVMGPEQG 115

Qy   129  FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
             |||||||||||||||||||||||||||||||||||||:  :|| |:
Db   116  VTLPGMTIVCGDSHTATHGAFGALAFGIGTSEVEHVLATQTLKQGRAKTMKIEVQGKAAP 175

Qy   189  GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD 248
             |:|:  :|   |: :|||:|||||||||:| |:|: |  ||:||||: |::|| :||
Db   176  GITAKDIVLAIIGKTGSAGGTGHVVEFCGEAIRDLSMEGRMTLCNMAIEMGAKAGLVAPD 235

Qy   249  EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP 308
             |||:|:||||||||   ::   |     |    ::|  ||: |:|:||||||||||||:
Db   236  ETTFNYVKGRLRHAPK--GKDFDDAVAYWKTLQTDEGATFDTVVTLQAEEISPQVTWGTNP 293

Qy   309  EDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIED 368
             |||||||:||:|:|||| |||||||||||||||||||||||:|||||||||||||||||
Db   294  GQVISVNDNIPDPASFADPVERASAEKALAYMGLKPGILLTEVAIDKVFIGSCTNSRIED 353

Qy   369  LRAAAAVVKGRKKAPNVKSAMVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGM 428
             |||||:||| |:|    ||| :||||||:|||:  ||||||:|||||||||||||||||
Db   354  LRAAAEIAKGRKVAPGVQ-ALVVPGSGPVKAQAEAEGLDKIFIEAGFEWRLPGCSMCLAM 412

Qy   429  NPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLIADVRKLT 481
             |: | |  |||||||||||||| |   :| ||: |: :|||:||: |:|:
Db   414  NDDRLGEWERCASTSNRNFEGRQRNGRTHLVSPAMAAAAGVFGKPVDIRDVT 466


RESULT 25
LEU2_ECO57
ID   LEU2_ECO57    STANDARD;    PRT;    465 AA.
AC   Q8XA00;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE   (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN   LEUC OR Z0081 OR ECS0076.
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
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RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
CC   -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC       and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC   -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC       H(2)O.
CC   -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC       isopropylmalate.
CC   -!- PATHWAY: Leucine biosynthesis; second step.
CC   -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC       SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics  and the EML outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long  as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AE005184; AAG54376.1; -.
DR   EMBL; AP002550; BAB33499.1; -.
DR   InterPro; IPR001030; Aconitase_N.
DR   InterPro; IPR004430; LeuC.
DR   Pfam; PF00330; aconitase; 1.
DR   PRINTS; PR00415; ACONITASE.
DR   ProDom; PD000511; Aconitase_N; 1.
DR   TIGRFAMs; TIGR00170; leuC; 1.
DR   PROSITE; PS00450; ACONITASE_1; 1.
DR   PROSITE; PS01244; ACONITASE_2; 1.
KW   Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT   INIT_MET        0      0                   BY SIMILARITY.
FT   METAL         346    346       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL         406    406       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL         409    409       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE    465 AA;  49766 MW;  72B977AE18AA2C41 CRC64;

Query Match            36.2%;  Score 1469.5;  DB 1;  Length 465;
Best Local Similarity  61.9%;  Pred. No. 5.9e-92;
Matches   292;  Conservative  59;  Mismatches 112;  Indels   9;  Gaps  4;

Qy     9  QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD 68
             :|||| :|: : |    :: |||| |||||||||||||||||: ||: |:|
Db     2  KTLYEKLFDAHVVYEAENETPLLYIDRHLVHEVTSPQAFDGLRAHGRPVRQPGKTFATMD 61

Qy    69  HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG 128
             ||||   :     :|| : ||   :|: ||  :|   |   :|    ||||||||||||
Db    62  HNVSTQT---KDINAC--GEMARIQMQELIKNCKEFGVELYDLNHPYQGIVHVMGPEQG 115

Qy   129  FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
             |||||||||||||||:|||||||||||||||||||||||||||||:||| |:|:|: |
Db   116  VTLPGMTIVCGDSHTATHGAFGALAFGIGTSEVEHVLATQTLKQGRAKTMKIEVQGKAAP 175

Qy   189  GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD 248
             |:|:  :|   |: :|||:|||||||||:| |:|: |  ||:||||: |::|| :||
Db   176  GITAKDIVLAIIGKTGSAGGTGHVVEFCGEAIRDLSMEGRMTLCNMAIEMGAKAGLVAPD 235

Qy   249  EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP 308
             |||:|:||||||||   ::   |     |    ::|  ||: |:|:||||||||||||:
Db   236  ETTFNYVKGRLRHAPK--GKDFDDAVAYWKTLQTDEGATFDTVVTLQAEEISPQVTWGTNP 293

Qy   309  EDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIED 368
             |||||||:||:|:|||| |||||||||||||||||||||||:|||||||||||||||||
Db   294  GQVISVNDNIPDPASFADPVERASAEKALAYMGLKPGILLTEVAIDKVFIGSCTNSRIED 353

Qy   369  LRAAAAVVKGRKKAPNVKSAMVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGM 428
             |||||:||| |:|    ||| :||||||:|||:  ||||||:|||||||||||||||||
Db   354  LRAAAEIAKGRKVAPGVQ-ALVVPGSGPVKAQAEAEGLDKIFIEAGFEWRLPGCSMCLAM 412
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Qy   429  NPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVNAAAAGIVGKLADVRKL  480
               | |:| ||||||||||||||||||||||| |||:|| ||||| :|   |||:| :
Db   413  NNDRLNPGERCASTSNRNFEGRQGRGGRTHLVSPAMAAAAVTGHFADIRNI  464
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Search completed: March 17, 2003, 08:49:29
Job time : 24 secs